

STIC-BioTech/ChemLib

195815

From: Ramirez, Delia
Sent: Monday, July 17, 2006 11:19 PM
To: STIC-BioTech/ChemLib
Subject: 10/716470

Hi,

I would like to request the following search: SEQ ID NO:10 in the protein databases (commercial & interference).

Thank you very much,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

CNFE

78701

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2006, 00:21:48 / Search time 202 Seconds
(without alignments)
280.668 Million cell updates/sec

Title: US-10-716-470-10

Perfect score: 620
Sequence: 1 NWIMEIFITGLIGASLLS.....EETPTVPDDTPLGVFGGH 124

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_8:*

- 1: geneseqp1980s:*
- 2: geneseqp1980s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	620	100.0	124	6	ABR58214
2	620	100.0	124	8	AD033791
3	620	100.0	124	8	AD037294
4	620	100.0	124	8	ADR89160
5	584	94.2	236	2	AAW37715
6	584	94.2	236	6	ABR58213
7	584	94.2	236	6	AD033789
8	584	94.2	236	8	AD033895
9	584	94.2	236	8	AD027292
10	584	94.2	236	8	ADR19717
11	584	94.2	236	8	ADR89158
12	576	92.9	236	8	AD033908
13	576	92.9	236	8	AD033908
14	571	92.1	233	4	AAU71888
15	571	92.1	233	4	ADB66197
16	571	92.1	233	7	ADB66197
17	389.5	62.8	231	4	AA664047
18	213	34.4	211	9	AB01789
19	213	34.4	211	9	AB01789
20	213	34.4	211	9	AB01789
21	213	34.4	211	9	AB01789
22	205	33.1	213	9	AB01789
23	185	29.8	214	7	ADP04687

24	176	28.4	208	6	ABM68839	Abm68839	Phototax
25	172.5	27.8	232	7	ABO75733	AbO75733	Pseudomon
26	170	27.4	199	7	ADG15729	ADG15729	M. tubercu
27	169	27.3	213	9	ABE35584	ABE35584	L. pneumo
28	165	26.6	201	9	ABE39976	ABE39976	L. pneumo
29	158	25.5	211	6	ADA34450	ADA34450	Acinetoba
30	112	18.1	211	9	ABM90714	ABM90714	M. xanthu
31	109	17.6	219	7	ABO61214	ABO61214	Klebsiell
32	104	16.8	212	8	AD051700	AD051700	Streptomy
33	101.5	16.4	205	5	ABM72206	ABM72206	Staphyloc
34	99.5	16.0	212	7	ADF04482	ADF04482	Bacterial
35	97	15.6	205	6	ABM67507	ABM67507	Phototax
36	97	15.6	222	9	ADA36962	ADA36962	S. tenjim
37	93.5	15.1	215	6	ADA36962	ADA36962	Actinoba
38	93	15.0	211	6	ABU19902	ABU19902	Protein e
39	91	14.7	111	2	AAW89961	AAW89961	Antigen f
40	91	14.7	210	2	AAW20426	AAW20426	H. pylori
41	91	14.7	215	2	AAW20968	AAW20968	H. pylori
42	91	14.7	252	8	ADY09559	ADY09559	Plant ful
43	90.5	14.6	208	6	ADA33824	ADA33824	Actinoba
44	88.5	14.3	212	3	ABO1787	ABO1787	Escherich
45	88.5	14.3	212	9	ABO7791	ABO7791	Escherich

ALIGNMENTS

RESULT 1
ABR58214 standard; protein; 124 AA.

AC	XX	ABR58214;	
DT	XX	23-OCT-2003 (revised)	
DT	XX	11-AUG-2003 (first entry)	
DE	XX	LySE24 protein.	
KM	XX	L-lysine; L-arginine; LySE24.	
OS	XX	Corynebacterium glutamicum.	
PN	XX	EP1266966-A2.	
PD	XX	18-DEC-2002.	
PF	XX	05-JUN-2002; 2002EP-00012539.	
PR	XX	12-JUN-2001; 2001JP-00177075.	
PA	XX	(AJIN) AJINOMOTO CO INC.	
PI	XX	Gunji Y, Yasueda H;	
DR	XX	WPI; 2003-241171/24.	
PS	XX	N-PSDB; ACC80942.	
PT	XX	Novel DNA encoding variant of LySE protein from a coryneform bacterium,	
PT	XX	when introduced into methanol assimilating bacterium, facilitates	
PT	XX	excretion of L-lysine and/or L-arginine to outside of a cell.	
PS	XX	Claim 8; Page 20; 23pp; English.	
CC	XX	The present invention relates to DNA encoding variants of protein with	
CC	XX	loop region and six hydrophobic helices which facilitates excretion of L-	
CC	XX	lysine and/or L-arginine to outside of cell of a methanol assimilating	
CC	XX	bacterium when introduced into the bacterium. The method is used for	
CC	XX	encoding a protein which facilitates excretion of L-lysine, L-arginine or	
CC	XX	both of these L-amino acids to outside of a cell of a methanol	
CC	XX	assimilating bacterium when DNA of the method is introduced into the	
CC	XX	bacterium. The present sequence represents a LySE24 protein from	
CC	XX	Brevibacterium lactofermentum. (Updated on 23-OCT-2003 to standardise OS	
CC	XX	field)	

XX Sequence 124 AA;
 SQ Query Match 100.0%; Score 620; DB 6; Length 124;
 Best Local Similarity 100.0%; Pred. No. 2.9e-68;
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MVMEIFITGLLGASLLSISGPQNVLYIKQIKREGILAVLVCLSDVFLFTAGTLGV 60
 1 MVMEIFITGLLGASLLSISGPQNVLYIKQIKREGILAVLVCLSDVFLFTAGTLGV 60
 61 DLISNAAPIVLDIMRWGIAVLLMFVAAKADMTNKVEAPQIIETEPTVPDDTPLGVF 120
 61 DLISNAAPIVLDIMRWGIAVLLMFVAAKADMTNKVEAPQIIETEPTVPDDTPLGVF 120
 121 GGCH 124
 121 GGCH 124

RESULT 2

ADO33791
 ID ADO33791 standard; procein; 124 AA.

ADO33791;
 12-AUG-2004 (first entry)

Corynebacterium glutamicum lysE (lysine export) mutant lysE24 protein.

lysE; lysine export; L-Lys production; L-Arg; methanol; mutant; mutein;
 lysE24.

Corynebacterium glutamicum.

Synthetic;

Key Location/Qualifiers

Misc-difference 119..124

/note="Replace wild-type residues 119-233 as a result of
 lysE24 mutation within coding DNA"

FR2847262-A1.

21-MAY-2004.

20-NOV-2003; 2003FR-00013575.

20-NOV-2002; 2002JP-00336340.

(AJIN) AJINOMOTO CO INC.

Gunji Y, Yasueda H;

WPI: 2004-403035/38.

N-PSDB; ADO33790.

Methylolacillus organism, useful for producing lysine and arginine,
 contains DNA encoding variant form of lysE protein that contains only the
 hydrophobic helices.

Claim 5; SEQ ID NO 10; 49pp; French.

The invention relates to a novel bacterium of the genus Methylolacillus
 that contains a DNA encoding a variant of the lysE (lysine export)
 protein and is able to produce L-Lys or L-Arg. The bacterium of the
 invention may be useful for production of L-Lys or L-Arg since
 incorporation of the lysE variant induces secretion of Lys and Arg, thus
 improving productivity. The bacterium can be grown on methanol, an
 inexpensive carbon source. The wild-type lysE protein is lethal to
 methanol-utilizing bacteria. The current sequence is that of the
 Corynebacterium glutamicum lysE (lysine export) mutant lysE24 protein of
 the invention.

SQ Sequence 124 AA;
 SQ Query Match 100.0%; Score 620; DB 8; Length 124;
 Best Local Similarity 100.0%; Pred. No. 2.9e-68;
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MVMEIFITGLLGASLLSISGPQNVLYIKQIKREGILAVLVCLSDVFLFTAGTLGV 60
 1 MVMEIFITGLLGASLLSISGPQNVLYIKQIKREGILAVLVCLSDVFLFTAGTLGV 60
 61 DLISNAAPIVLDIMRWGIAVLLMFVAAKADMTNKVEAPQIIETEPTVPDDTPLGVF 120
 61 DLISNAAPIVLDIMRWGIAVLLMFVAAKADMTNKVEAPQIIETEPTVPDDTPLGVF 120
 121 GGCH 124
 121 GGCH 124

RESULT 3

ADO27294
 ID ADO27294 standard; protein; 124 AA.

ADO27294;

12-AUG-2004 (first entry)

Mutant Corynebacterium glutamicum truncated lysE protein Segid 10.

Entner-Doudoroff pathway; methanol metabolism;

6-phosphogluconate dehydratase; EDP;

2-keto-3-deoxy-6-phosphogluconate aldolase; EDA; L-amino acid;

agriculture; food industry; lysE; mutant; mutein.

Corynebacterium glutamicum.

Synthetic.

FR2847265-A1.

21-MAY-2004.

20-NOV-2003; 2003FR-00013576.

20-NOV-2002; 2002JP-00336346.

(AJIN) AJINOMOTO CO INC.

Gunji Y, Yasueda H;

WPI: 2004-403038/38.

N-PSDB; ADO27293.

Microbial production of amino acids, useful in agriculture and foods,
 comprises growing bacteria that use the Entner-Doudoroff pathway for
 methanol metabolism and have increased activity of enzymes in this
 pathway.

Disclosure; SEQ ID NO 10; 51pp; French.

This invention relates to the novel production of L-amino acids from
 microorganisms that use the Entner-Doudoroff pathway for methanol
 metabolism, such that L-residues are secreted into and recovered from the
 culture medium. Specifically, it refers to an increase in the activity of
 two enzymes, namely 6-phosphogluconate dehydratase (EDP) and/or 2-keto-3-
 deoxy-6-phosphogluconate aldolase (EDA) that improve production of
 certain amino acids from an inexpensive carbon source. The present
 invention describes the production of L-amino acids from a biosynthetic
 pathway that uses pyruvic acid as an intermediate. Accordingly, this
 method can be used to produce lysine, leucine, isoleucine and valine,
 which are amino acids applicable to the agricultural and food industries.
 This polypeptide sequence is the mutant Corynebacterium glutamicum lysE
 protein containing an in frame stop codon that truncates the protein
 prematurely, given in an exemplification of the invention.

XX Sequence 124 AA;
SQ Query Match 100.0%; Score 620; DB 8; Length 124;
Best Local Similarity 100.0%; Pred. No. 2.9e-68;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWIMEIFITGLLGASLLSIGPQNVIVIKQIKREGIAVLVCLISDVFLFIAGTLGV 60
DB 1 MWIMEIFITGLLGASLLSIGPQNVIVIKQIKREGIAVLVCLISDVFLFIAGTLGV 60
QY 61 DLSNNAPIVLDIMRWGIAVLLMFPAVMAKADMTNKVEAPQIIIEETPTVPDDTPLGVF 120
DB 61 DLSNNAPIVLDIMRWGIAVLLMFPAVMAKADMTNKVEAPQIIIEETPTVPDDTPLGVF 120
QY 121 GGGH 124
DB 121 GGGH 124

RESULT 4
ADR89160
ID ADR89160 standard; protein; 124 AA.
XX ADR89160;
AC ADR89160;
XX 18-NOV-2004 (first entry)
DT 18-NOV-2004 (first entry)
XX Amino acid sequence of a mutant lysE gene fragment.
DE lysine decarboxylase; enzyme; ldc gene; cadaverine; L-lysine;
XX lysine production; lysE gene.
KM Corynebacterium glutamicum.
XX Synthetic.
OS FR2851575-A1.
XX 27-AUG-2004.
PD 25-FEB-2004; 2004FR-00001873.
XX 25-FEB-2003; 2003JP-00047185.
XX (AJIN) AJINOMOTO CO INC.
XX Hirano S, Yasueda H;
XX WPI; 2004-618218/60.
DR N-PSDB; ADR89159.

PT Preparation of L-lysine by growing Methylobionas in which the endogenous
PT lysine decarboxylase gene has been inactivated, also new lysine
PT decarboxylase and nucleic acid encoding it.
XX Example 4; SEQ ID NO 24; 57bp; French.
PS The specification describes a lysine decarboxylase enzyme of
XX Methylobionas methylotrophus. The lysine decarboxylase gene is designated
CC ldc gene. The lysine decarboxylase enzyme decomposes lysine to
CC cadaverine. M. methylotrophus cells in which this gene has been reduced
CC or eliminated are useful for fermentative production of L-lysine in
CC methanol-based media. Inactivation of the enzyme increases the efficiency
CC of lysine production in Methylobionas cells. The present sequence is
CC encoded by a mutated lysE gene fragment, with a thymine inserted after
CC guanine 355. This fragment was used to construct a plasmid which was then
CC used to produce L-lysine in cells containing an interrupted ldc gene.
XX Sequence 124 AA;
SQ Query Match 100.0%; Score 620; DB 8; Length 124;
Best Local Similarity 100.0%; Pred. No. 2.9e-68;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWIMEIFITGLLGASLLSIGPQNVIVIKQIKREGIAVLVCLISDVFLFIAGTLGV 60
DB 1 MWIMEIFITGLLGASLLSIGPQNVIVIKQIKREGIAVLVCLISDVFLFIAGTLGV 60
QY 61 DLSNNAPIVLDIMRWGIAVLLMFPAVMAKADMTNKVEAPQIIIEETPTVPDDTPLGVF 120
DB 61 DLSNNAPIVLDIMRWGIAVLLMFPAVMAKADMTNKVEAPQIIIEETPTVPDDTPLGVF 120
QY 121 GGGH 124
DB 121 GGGH 124

RESULT 5
AAW37715
ID AAW37715 standard; protein; 236 AA.
XX AAW37715;
AC AAW37715;
XX 12-MAR-1998 (first entry)
DT 12-MAR-1998 (first entry)
XX C. glutamicum Lys E protein (lysine export protein).
DE LysE; lysE; ORF3; lysine transport; regulatory protein; export protein;
XX Microbial production; amino acid; animal feed additive.
KM Corynebacterium glutamicum.
XX DE19548222-A1.
XX 26-JUN-1997.
PD 22-DEC-1995; 95DE-01048222.
XX 22-DEC-1995; 95DE-01048222.
XX (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX Vrijic M, Eggeling L, Sahm H;
XX WPI; 1997-333867/31.
DR N-PSDB; AAT96816.

PT Increasing microbial production of amino acids, especially lysine - by
PT improving export carrier activity or corresponding gene expression, also
PT new export and regulatory genes from Corynebacterium.
XX Claim 42; Page 10; 16pp; German.
PS This sequence is the lysE protein product, a lysine export protein. LysE
CC and lysE encode a lysine transport regulatory protein and an export
CC protein, respectively. Microbial production of amino acids (A) is
CC improved by increasing the export-carrier activity and/or the export gene
CC expression in a microorganism that produces (A). The method is
CC specifically used to increase production of lysine, used as an animal
CC feed additive. Other (A) are variously useful as pharmaceuticals,
CC condiments and intermediates for fine chemicals. This method increases
CC the amount of (A) secreted into the culture medium. Export of (A) has
CC been found to depend on a single gene
XX Sequence 236 AA;
SQ Query Match 94.2%; Score 584; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWIMEIFITGLLGASLLSIGPQNVIVIKQIKREGIAVLVCLISDVFLFIAGTLGV 60
DB 1 MWIMEIFITGLLGASLLSIGPQNVIVIKQIKREGIAVLVCLISDVFLFIAGTLGV 60
QY 61 DLSNNAPIVLDIMRWGIAVLLMFPAVMAKADMTNKVEAPQIIIEETPTVPDDTPLGV 118

DB 61 DLLSNAPIVLDIMRWGIAVLLMFVMAKADMTNKVEAPQIIEETPTVPDDTPLG 118

RESULT 6
AAG93201
ID AAG93201 standard; procein; 236 AA.
XX
AC AAG93201;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum protein fragment SEQ ID NO: 6955.
XX
KM Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
XX
OS Corynebacterium glutamicum.
XX
PN EPI108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-00127688.
XX
PR 16-DEC-1999; 99JP-00377484.
XX
PR 07-APR-2000; 2000JP-00159162.
XX
PR 03-AUG-2000; 2000JP-00280988.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
XX
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
DR WPI; 2001-376931/40.
XX
DR N-PSDB; AAH68420.
XX
PT Novel polynucleotides derived from Coryneform bacteria, for identifying
XX
PT mutation point of a gene, measuring expression of a gene, analyzing
XX
PT expression profile or pattern of a gene and identifying homologous gene.
XX
PS Claim 29; SEQ ID NO 6955; 246bp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
XX
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
XX
CC are useful for identifying the mutation point of a gene derived from a
XX
CC mutant of coryneform bacterium, measuring expression amount and analyzing
XX
CC the expression profile or expression pattern of a gene derived from
XX
CC Coryneform bacterium, and identifying a homologue of a gene derived from
XX
CC Coryneform bacterium. Coryneform bacteria are useful for producing amino
XX
CC acids, nucleic acids, vitamins, saccharides and organic acids,
XX
CC particularly L-lysine. The present sequence is a protein described in the
XX
CC exemplification of the invention. Note: The sequence data for this patent
XX
CC did not form part of the printed specification, but was obtained in
XX
CC electronic format directly from the European Patent Office

XX
SQ Sequence 236 AA;
XX
Query Match 94.2%; Score 584; DB 4; Length 236;
XX
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
XX
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTMEIFITGLLIGASLLSIGPQNVLVIKGIRKGLIAVLLVCLISDVFLFIAGTLGV 60
DB 1 MVTMEIFITGLLIGASLLSIGPQNVLVIKGIRKGLIAVLLVCLISDVFLFIAGTLGV 60
QY 61 DLLSNAPIVLDIMRWGIAVLLMFVMAKADMTNKVEAPQIIEETPTVPDDTPLG 118
DB 61 DLLSNAPIVLDIMRWGIAVLLMFVMAKADMTNKVEAPQIIEETPTVPDDTPLG 118

RESULT 7
ABR58213
ID ABR58213 standard; protein; 236 AA.

XX
AC ABR58213;
XX
DT 23-OCT-2003 (revised)
XX
DT 11-AUG-2003 (first entry)
XX
DE LysE protein.
XX
KM L-lysine; L-arginine; LysE.
XX
OS Corynebacterium glutamicum.
XX
PN EPI266966-A2.
XX
PD 18-DEC-2002.
XX
PF 05-JUN-2002; 2002EP-00012539.
XX
PR 12-JUN-2001; 2001JP-00177075.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Gunji Y, Yasueda H;
XX
XX
DR WPI; 2003-241171/24.
XX
DR N-PSDB; ACC80941.
XX
PT Novel DNA encoding variant of LysE protein from a coryneform bacterium,
XX
PT when introduced into methanol assimilating bacterium, facilitates
XX
PS excretion of L-lysine and/or L-arginine to outside of a cell.
XX
PS Disclosure; Page 18-19; 23pp; English.
XX
CC The present invention relates to DNA encoding variants of protein with
XX
CC loop region and six hydrophobic helices which facilitates excretion of L-
XX
CC lysine and/or L-arginine to outside of cell of a methanol assimilating
XX
CC bacterium when introduced into the bacterium. The method is used for
XX
CC encoding a protein which facilitates excretion of L-lysine, L-arginine or
XX
CC both of these L-amino acids to outside of a cell of a methanol
XX
CC assimilating bacterium when DNA of the method is introduced into the
XX
CC bacterium. The present sequence represents a LysE protein from
XX
CC Brevibacterium lactofermentum. (Updated on 23-Oct-2003 to standardise OS
XX
CC field)

XX
SQ Sequence 236 AA;
XX
Query Match 94.2%; Score 584; DB 6; Length 236;
XX
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
XX
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTMEIFITGLLIGASLLSIGPQNVLVIKGIRKGLIAVLLVCLISDVFLFIAGTLGV 60
DB 1 MVTMEIFITGLLIGASLLSIGPQNVLVIKGIRKGLIAVLLVCLISDVFLFIAGTLGV 60
QY 61 DLLSNAPIVLDIMRWGIAVLLMFVMAKADMTNKVEAPQIIEETPTVPDDTPLG 118
DB 61 DLLSNAPIVLDIMRWGIAVLLMFVMAKADMTNKVEAPQIIEETPTVPDDTPLG 118

RESULT 8
ADO33789
ID ADO33789 standard; protein; 236 AA.
XX
AC ADO33789;
XX
DT 12-AUG-2004 (first entry)
XX
DE Corynebacterium glutamicum LysE (lysine export) wild-type protein.
XX
KM LysE; lysine export; L-Lys production; L-Arg; methanol; wild-type.
XX
OS Corynebacterium glutamicum.
XX

PN FR2847262-A1.
XX
XX
PD 21-MAY-2004.
XX
PF 20-NOV-2003; 2003FR-00013575.
XX
PR 20-NOV-2002; 2002JP-00336340.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Gunji Y, Yasueda H;
XX
XX WPI; 2004-403035/38.
DR N-PSDB; ADO33788.
XX
XX
PT Methylobacillus organism, useful for producing lysine and arginine,
PT contains DNA encoding variant form of LysE protein that contains only the
PT hypotrophic helices.
XX
XX Example 1; SEQ ID NO 8; 49pp; French.
XX
XX The invention relates to a novel bacterium of the genus Methylobacillus
CC that contains a DNA encoding a variant of the LysE (lysine export)
CC protein and is able to produce L-Lys or L-Arg. The bacterium of the
CC invention may be useful for production of L-Lys or L-Arg since
CC incorporation of the LysE variant induces secretion of Lys and Arg, thus
CC improving productivity. The bacterium can be grown on methanol, an
CC inexpensive carbon source. The wild-type LysE protein is lethal to
CC methanol-utilising bacteria. The current sequence is that of the
CC Corynebacterium glutamicum LysE (lysine export) wild-type protein of the
CC invention.
XX
XX Sequence 236 AA;
SQ
Query Match 94.2%; Score 584; DB 8; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVIMEIFITGLLGLASLLSIGPONVLVIKQIKREGIAYLVLCISDVLEFIFTAGTIGV 60
Db 1 MVIMEIFITGLLGLASLLSIGPONVLVIKQIKREGIAYLVLCISDVLEFIFTAGTIGV 60
QY 61 DLISNAAPIVLDINRWGSIAYLWFAVMAAKDAMTNKVEAPQIIEETPTVPDDTPLG 118
Db 61 DLISNAAPIVLDINRWGSIAYLWFAVMAAKDAMTNKVEAPQIIEETPTVPDDTPLG 118
RESULT 9
ADO33895
ID ADO33895 standard; protein; 236 AA.
XX
AC ADO33895;
XX
XX 12-AUG-2004 (first entry)
XX
XX Corynebacterium glutamicum LysE (lysine export) wild-type protein.
XX
XX LysE; lysine export; methanol-utilising bacterium;
KM S-(2-aminoethyl)cysteine resistance; arginine export; wild-type.
XX
XX Corynebacterium glutamicum.
OS
XX FR2847264-A1.
XX
XX 21-MAY-2004.
XX
XX 20-NOV-2003; 2003FR-00013574.
XX
XX 20-NOV-2002; 2002JP-00336315.
XX
XX (AJIN) AJINOMOTO CO INC.
PA
XX Gunji Y, Yasueda H;
PI

XX
XX
DR WPI; 2004-403037/38.
DR N-PSDB; ADO33894.
XX
XX
XX New DNA encoding mutant form of LysE protein, useful for transformation
PT of methanol-utilizing bacteria for production of lysine and arginine,
PT also new transformants.
XX
XX
PS Claim 1; SEQ ID NO 2; 52pp; French.
XX
XX The invention relates to a novel DNA that encodes a mutant of the LysE
CC (lysine export) protein of a coryneform bacterium, or its homologue, in
CC which at least Gly56 has been replaced by a different amino acid and
CC where the introduction of the DNA into a methanol-utilising bacterium
CC confers resistance to a lysine analogue such as S-(2-aminoethyl)cysteine.
CC The DNA of the invention may be useful since its introduction induces
CC export of Lys and/or Arg from cells, thus facilitating production of
CC these amino acids from an inexpensive carbon source and increasing their
CC concentration in the extracellular medium. The wild-type LysE sequence is
CC not functional in methanol-utilising bacteria. The current sequence is
CC that of the Corynebacterium glutamicum LysE (lysine export) wild-type
CC protein of the invention.
XX
XX Sequence 236 AA;
SQ
Query Match 94.2%; Score 584; DB 8; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVIMEIFITGLLGLASLLSIGPONVLVIKQIKREGIAYLVLCISDVLEFIFTAGTIGV 60
Db 1 MVIMEIFITGLLGLASLLSIGPONVLVIKQIKREGIAYLVLCISDVLEFIFTAGTIGV 60
QY 61 DLISNAAPIVLDINRWGSIAYLWFAVMAAKDAMTNKVEAPQIIEETPTVPDDTPLG 118
Db 61 DLISNAAPIVLDINRWGSIAYLWFAVMAAKDAMTNKVEAPQIIEETPTVPDDTPLG 118
RESULT 10
ADO27292
ID ADO27292 standard; protein; 236 AA.
XX
XX ADO27292;
XX
XX 12-AUG-2004 (first entry)
XX
XX Corynebacterium glutamicum LysE protein Segid 8.
XX
XX Entner-Doudoroff pathway; methanol metabolism;
DE 6-phosphogluconate dehydratase; EBD;
XX 2-keto-3-deoxy-6-phosphogluconate aldolase; EDA; L-amino acid;
XX agriculture; Food industry; LysE.
XX
XX Corynebacterium glutamicum.
OS
XX FR2847265-A1.
XX
XX 21-MAY-2004.
XX
XX 20-NOV-2003; 2003FR-00013576.
XX
XX 20-NOV-2002; 2002JP-00336346.
XX
XX (AJIN) AJINOMOTO CO INC.
PA
XX Gunji Y, Yasueda H;
XX
XX WPI; 2004-403038/38.
DR N-PSDB; ADO27291.
XX
XX
XX Microbial production of amino acids, useful in agriculture and foods,
PT comprises growing bacteria that use the Entner-Doudoroff pathway for
PT methanol metabolism and have increased activity of enzymes in this

PT pathway.
 XX
 PS Disclosure; SEQ ID NO 8; s1pp; French.
 XX
 CC This invention relates to the novel production of L-amino acids from
 CC microorganisms that use the Entner-Doudoroff pathway for methanol
 CC metabolism, such that L-residues are secreted into and recovered from the
 CC culture medium. Specifically, it refers to an increase in the activity of
 CC two enzymes, namely 6-phosphogluconate dehydratase (EDD) and/or 2-keto-3
 CC -deoxy-6-phosphogluconate aldolase (EDA) that improve production of
 CC certain amino acids from an inexpensive carbon source. The present
 CC invention describes the production of L-amino acids from a biosynthetic
 CC pathway that uses pyruvic acid as an intermediate. Accordingly, this
 CC method can be used to produce lysine, leucine, isoleucine and valine,
 CC which are amino acids applicable to the agricultural and food industries.
 CC This polypeptide sequence is the Corynebacterium glutamicum lysE protein
 CC given in an exemplification of the invention.
 CC
 SQ Sequence 236 AA;
 Query Match 94.2%; Score 584; DB 8; Length 236;
 Best Local Similarity 100.0%; Pred. No. 1.9e-63;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVIMEIFITGLLGASLLSIGPQNVLYIKGIRKREGLIALLVCLISDVFLFIAGTLGV 60
 DB 1 MVIMEIFITGLLGASLLSIGPQNVLYIKGIRKREGLIALLVCLISDVFLFIAGTLGV 60
 QY 61 DLISNAPIVLDIMRWGIAVLLMFVMAAKDAMTKNVEAPQIIETEPTVPDDTPIG 118
 DB 61 DLISNAPIVLDIMRWGIAVLLMFVMAAKDAMTKNVEAPQIIETEPTVPDDTPIG 118
 RESULT 11
 ADRI9717
 ID ADRI9717 standard; protein; 236 AA.
 XX
 AC ADRI9717;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE lysE amino acid sequence, seq id 18.
 XX
 KM L-lysine; bacteria; methanol; L-methionine; Methylophilus bacteria; meta;
 KM homoserine o-acetyltransferase; lysE.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN FR2850394-A1.
 XX
 PD 30-JUL-2004.
 XX
 PF 29-JAN-2004; 2004FR-00000816.
 XX
 PR 29-JAN-2003; 2003JP-00020513.
 XX
 PA (AJIN) AJINOMOTO CO INC.
 XX
 DR MPI; 2004-563572/55.
 DR N-PADB; ADRI9716.
 XX
 PT L-Lysine preparation with high productivity, by culturing methanol-
 PT utilizing bacteria auxotrophic for L-methionine, preferably new
 PT Methylophilus strains.
 XX
 PS Disclosure; SEQ ID NO 18; 43pp; French.
 XX
 CC The invention relates to the production of L-lysine (I). The method
 CC involves culturing bacteria which utilize methanol, require L-methionine
 CC (II) for growth and produce (I) in a medium containing methanol as the
 CC main carbon source, then recovering the (I) accumulated in the culture.
 CC disclosed are Methylophilus bacteria which require (II) for growth and
 CC produce (I). Methylophilus bacteria requiring (II) for growth are

CC obtained by mutation of wild strains using physical stimuli, or
 CC preferably a chemical mutagen, or by using genetic engineering methods to
 CC suppress the activity of an enzyme involved in the synthesis of (II),
 CC e.g. by cleaving the gene meta (encoding homoserine o-acetyltransferase)
 CC in Methylophilus methylotrophus. The invention is useful in the
 CC production of L-lysine. L-lysine is obtained with high efficacy from
 CC bacteria utilizing (inexpensive) methanol as carbon source. The current
 CC sequence represents the lysE amino acid sequence.
 CC
 SQ Sequence 236 AA;
 Query Match 94.2%; Score 584; DB 8; Length 236;
 Best Local Similarity 100.0%; Pred. No. 1.9e-63;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVIMEIFITGLLGASLLSIGPQNVLYIKGIRKREGLIALLVCLISDVFLFIAGTLGV 60
 DB 1 MVIMEIFITGLLGASLLSIGPQNVLYIKGIRKREGLIALLVCLISDVFLFIAGTLGV 60
 QY 61 DLISNAPIVLDIMRWGIAVLLMFVMAAKDAMTKNVEAPQIIETEPTVPDDTPIG 118
 DB 61 DLISNAPIVLDIMRWGIAVLLMFVMAAKDAMTKNVEAPQIIETEPTVPDDTPIG 118
 RESULT 12
 ADRI9158
 ID ADRI9158 standard; protein; 236 AA.
 XX
 AC ADRI9158;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Amino acid sequence of a wild type lysE gene.
 XX
 KM lysine decarboxylase; enzyme; ldc gene; lysine; cadaverine; L-lysine;
 KM lysine production; lysE gene.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN FR2851575-A1.
 XX
 PD 27-AUG-2004.
 XX
 PF 25-FEB-2004; 2004FR-00001873.
 XX
 PR 25-FEB-2003; 2003JP-00047185.
 XX
 PA (AJIN) AJINOMOTO CO INC.
 XX
 PI Hirano S, Yasueda H;
 XX
 DR MPI; 2004-618218/60.
 DR N-PADB; ADRI9157.
 XX
 PT Preparation of L-lysine by growing Methylomonas in which the endogenous
 PT lysine decarboxylase gene has been inactivated, also new lysine
 PT decarboxylase and nucleic acid encoding it.
 XX
 PS Example 4; SEQ ID NO 22; 57pp; French.
 XX
 CC The specification describes a lysine decarboxylase enzyme of
 CC Methylophilus methylotrophus. The lysine decarboxylase gene is designated
 CC ldc gene. The lysine decarboxylase enzyme decomposes lysine to
 CC cadaverine. M. methylotrophus cells in which this gene has been reduced
 CC or eliminated are useful for fermentative production of L-lysine in
 CC methanol-based media. Inactivation of the enzyme increases the efficiency
 CC of lysine production in Methylophilus cells. The present sequence is
 CC encoded by a lysE gene fragment. This fragment was used to construct a
 CC plasmid which was then used to produce L-lysine in cells containing an
 CC interrupted ldc gene.
 XX
 SQ Sequence 236 AA;

PR 27-AUG-1999; 99DE-01040764.
 PR 27-AUG-1999; 99DE-01040765.
 PR 27-AUG-1999; 99DE-01040766.
 PR 27-AUG-1999; 99DE-01040832.
 PR 31-AUG-1999; 99DE-01041378.
 PR 31-AUG-1999; 99DE-01041379.
 PR 31-AUG-1999; 99DE-01041380.
 PR 31-AUG-1999; 99DE-01041394.
 PR 31-AUG-1999; 99DE-01041396.
 PR 03-SEP-1999; 99DE-01042076.
 PR 03-SEP-1999; 99DE-01042077.
 PR 03-SEP-1999; 99DE-01042079.
 PR 03-SEP-1999; 99DE-01042086.
 PR 03-SEP-1999; 99DE-01042087.
 PR 03-SEP-1999; 99DE-01042088.
 PR 03-SEP-1999; 99DE-01042095.
 PR 03-SEP-1999; 99DE-01042124.
 PR 03-SEP-1999; 99DE-01042129.
 PR 09-MAR-2000; 2000US-0187970P.
 XX
 XX (BADI) BASF AG.
 XX
 XX Pompejus M, Kroegeer B, Schroeder H, Zelder O, Haberhauer G;
 XX WPI; 2001-137957/14.
 DR N-PSDB; AAF71779.
 XX
 XX Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway
 PT proteins, useful for producing fine chemicals in microorganisms,
 PT including organic acids, nonproteinogenic amino acids, and purine and
 PT pyrimidine bases.
 XX
 PS Claim 20; Page 234-235; 1737pp; English.
 XX
 CC AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic
 CC pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP
 CC nucleic acids are useful for the production of fine chemicals in
 CC microorganisms, including organic acids, nonproteinogenic amino acids,
 CC purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated
 CC and unsaturated fatty acids, diols, carbohydrates, aromatic compounds,
 CC vitamins, cofactors, polyelectrolytes and enzymes
 CC
 XX Sequence 233 AA;
 SQ
 QY Query Match 92.1%; Score 571; DB 4; Length 233;
 Best Local Similarity 100.0%; Pred. No. 7,6e-62;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 4 MEIFITGLLGASLLSIGPQNVLYIKQIKREGGLAVLVCLISDVFLFIAGTLGVDLL 63
 1 MEIFITGLLGASLLSIGPQNVLYIKQIKREGGLAVLVCLISDVFLFIAGTLGVDLL 60
 QY 64 SNAAPITVDIMRWGIAIYLLMFAPVMAAKDAMTKVKEAPQIIETETPTVDDTFLG 118
 61 SNAAPITVDIMRWGIAIYLLMFAPVMAAKDAMTKVKEAPQIIETETPTVDDTFLG 115
 Db
 RESULT 15
 AAU71888
 ID AAU71888 standard; protein: 233 AA.
 XX
 AC AAU71888;
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE C. glutamicum metabolic pathway protein encoded by gene #23.
 XX
 KM Metabolic pathway protein; MP; lysine biosynthesis pathway;
 KM methionine biosynthesis pathway; large-scale production of fine chemical;
 KM Corynebacterium diptheriae; diptheria.
 OS Corynebacterium glutamicum.

PN WO20016573-A2.
 XX
 PD 13-SEP-2001.
 XX
 XX 22-DEC-2000; 2000WO-IB002035.
 XX
 FF 09-MAR-2000; 2000US-0187970P.
 PR 23-JUN-2000; 2000US-00606740.
 XX
 XX (BADI) BASF AG.
 XX
 XX Pompejus M, Kroegeer B, Schroeder H, Zelder O, Haberhauer G;
 PI Kim J, Lee H, Hwang B;
 XX WPI; 2001-582269/65.
 DR N-PSDB; AAS96098.
 XX
 PT Nucleic acids encoding metabolic pathway proteins from Corynebacterium
 PT glutamicum, useful for producing methionine and lysine in Corynebacterium
 PT and Brevibacterium.
 PT
 XX Disclosure; Page 215-216; 316pp; English.
 XX
 XX The present invention relates to the isolation of novel Corynebacterium
 CC glutamicum genes (AAS96073-AAS96132) encoding metabolic pathway (MP)
 CC proteins. The metabolic pathway proteins of the invention include enzymes
 CC involved in the lysine and methionine biosynthetic pathway. The
 CC polynucleotide sequences of the invention can be used for the large-scale
 CC production and/or modulation of expression of fine chemicals such as
 CC lysine and methionine. The sequences of the invention may be used to
 CC identify C. glutamicum and related organisms e.g. C. diptheriae in a
 CC subject to detect diptheria. AAU71863-AAU71922 represent the novel C.
 CC glutamicum metabolic pathway proteins of the invention
 CC
 XX Sequence 233 AA;
 SQ
 QY Query Match 92.1%; Score 571; DB 4; Length 233;
 Best Local Similarity 100.0%; Pred. No. 7,6e-62;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 4 MEIFITGLLGASLLSIGPQNVLYIKQIKREGGLAVLVCLISDVFLFIAGTLGVDLL 63
 1 MEIFITGLLGASLLSIGPQNVLYIKQIKREGGLAVLVCLISDVFLFIAGTLGVDLL 60
 QY 64 SNAAPITVDIMRWGIAIYLLMFAPVMAAKDAMTKVKEAPQIIETETPTVDDTFLG 118
 61 SNAAPITVDIMRWGIAIYLLMFAPVMAAKDAMTKVKEAPQIIETETPTVDDTFLG 115
 Db
 Search completed: July 19, 2006, 00:25:26
 Job time : 206 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2006, 00:42:58 ; Search time 188 seconds
(without alignments)
305.525 Million cell updates/sec

Title: US-10-716-470-10

Perfect score: 620

Sequence: 1 MVMEIFITGLLGASLLS.....ETETPTVDDTLPGLGVGGGH 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	620	100.0	124	4 US-10-166-142-10	Sequence 10, Appl
2	620	100.0	124	4 US-10-716-473-10	Sequence 10, Appl
3	620	100.0	124	5 US-10-784-986-24	Sequence 24, Appl
4	620	100.0	124	5 US-10-716-470-10	Sequence 10, Appl
5	584	94.2	236	3 US-09-738-626-6955	Sequence 6955, Ap
6	584	94.2	236	4 US-10-166-142-8	Sequence 8, Appl
7	584	94.2	236	4 US-10-716-473-8	Sequence 8, Appl
8	584	94.2	236	4 US-10-716-480A-2	Sequence 2, Appl
9	584	94.2	236	4 US-10-760-283-18	Sequence 18, Appl
10	584	94.2	236	5 US-10-784-986-22	Sequence 22, Appl
11	584	94.2	236	5 US-10-716-470-8	Sequence 8, Appl
12	571	92.1	233	5 US-09-746-660A-52	Sequence 52, Appl
13	571	92.1	233	4 US-10-166-232-25	Sequence 25, Appl
14	571	92.1	233	4 US-10-858-730-25	Sequence 25, Appl
15	571	92.1	233	6 US-11-055-822-34	Sequence 34, Appl
16	571	92.1	233	6 US-11-239-674-52	Sequence 52, Appl
17	571	92.1	233	6 US-11-116-286-16	Sequence 16, Appl
18	213	34.4	211	5 US-10-858-730-93	Sequence 93, Appl
19	170	27.4	199	5 US-10-858-730-93	Sequence 237, App
20	154	24.8	201	5 US-10-858-730-94	Sequence 94, Appl
21	149	24.0	204	5 US-10-858-730-95	Sequence 94, Appl
22	140	22.6	203	4 US-10-156-761-8659	Sequence 95, Appl
23	104	16.8	211	4 US-10-374-903A-6	Sequence 6, Appl
24	93	15.0	212	4 US-10-282-122A-47826	Sequence 47826, A
25	91	14.7	210	4 US-10-335-977-5883	Sequence 5883, Ap
26	91	14.7	210	4 US-10-335-977-5884	Sequence 5884, Ap
27	91	14.7	215	4 US-10-335-977-5885	Sequence 5885, Ap

28	91	14.7	226	4 US-10-425-115-323683	Sequence 323683,
29	91	14.7	252	4 US-10-425-114-65374	Sequence 65374, A
30	89.5	14.4	202	5 US-10-858-730-96	Sequence 96, Appl
31	88.5	14.3	212	6 US-11-116-286-12	Sequence 12, Appl
32	88	14.2	212	6 US-09-738-626-3665	Sequence 3665, Ap
33	85.5	13.8	224	3 US-10-156-761-7796	Sequence 7796, Ap
34	80	12.9	452	6 US-10-096-568A-22692	Sequence 22692, A
35	80	12.9	463	4 US-10-425-115-349872	Sequence 349872,
36	80	12.9	469	4 US-10-425-114-50691	Sequence 50691, A
37	80	12.9	484	6 US-11-096-568A-22691	Sequence 22691, A
38	79.5	12.8	205	3 US-09-927-395-2	Sequence 2, Appl1
39	79.5	12.8	205	3 US-09-847-392-2	Sequence 2, Appl1
40	79.5	12.8	205	6 US-11-106-455-2	Sequence 2, Appl1
41	79.5	12.8	205	6 US-11-091-889-2	Sequence 2, Appl1
42	79.5	12.8	205	6 US-11-091-889-2	Sequence 2, Appl1
43	79.5	12.8	386	5 US-10-954-778-87	Sequence 87, Appl
44	77.5	12.5	195	4 US-10-620-487-2	Sequence 2, Appl1
45	77.5	12.5	195	6 US-11-116-286-14	Sequence 14, Appl

ALIGNMENTS

```

RESULT 1
US-10-166-142-10
; Sequence 10, Application US/10166142
; Publication No. US20030124687A1
; GENERAL INFORMATION:
; APPLICANT: GUNJI, YOSHIDA
; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL
; FILE REFERENCE: 223789US
; CURRENT APPLICATION NUMBER: US/10/166,142
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: JP 2001-177075
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Brevibacterium lactofermentum
US-10-166-142-10

Query Match      100.0%; Score 620; DB 4; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MVMEIFITGLLGASLLSISGPONVLVIKQIGREGIAVLVCLISDVFLTAGTLGV 60
      |||
DB      1 MVMEIFITGLLGASLLSISGPONVLVIKQIGREGIAVLVCLISDVFLTAGTLGV 60
      |||

QY      61 DLSNAPVIVDIRMGIAVLVFAVMAKADANTNKVEAPQIETETPTVDDTLPGLGV 120
      |||
DB      61 DLSNAPVIVDIRMGIAVLVFAVMAKADANTNKVEAPQIETETPTVDDTLPGLGV 120
      |||

QY      121 GGGH 124
      |||
DB      121 GGGH 124
      |||

RESULT 2
US-10-716-473-10
; Sequence 10, Application US/10716473
; Publication No. US20040142435A1
; GENERAL INFORMATION:
; APPLICANT: Ajinomoto Co. Inc.
; TITLE OF INVENTION: Method for Producing L-Amino Acid Using Methyloctroph
; FILE REFERENCE: OP1629
; CURRENT APPLICATION NUMBER: US/10/716,473
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: JP 2002-336346

```

PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Brevibacterium lactofermentum
US-10-716-473-10

Query Match 100.0%; Score 620; DB 4; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTMEIFITGLLIGASLLSIGPQNVLVIKQIKREGIAVLVCLISDVFLFIAGTLGV 60
DB 1 MVTMEIFITGLLIGASLLSIGPQNVLVIKQIKREGIAVLVCLISDVFLFIAGTLGV 60
QY 61 DLISNAPIVLDIMRWGIAVILMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPIGVF 120
DB 61 DLISNAPIVLDIMRWGIAVILMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPIGVF 120
QY 121 GGCH 124
DB 121 GGCH 124

RESULT 3
US-10-784-986-24
; Sequence 24, Application US/10784986
; Publication No. US20040229311A1
; GENERAL INFORMATION:
; APPLICANT: HIRANO, Seiko
; TITLE OF INVENTION: Novel lysine decarboxylase gene and method for
; FILE REFERENCE: US-109
; CURRENT APPLICATION NUMBER: US/10/784,986
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: JP 2003-47185
; PRIOR FILING DATE: 2003-02-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 24
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Brevibacterium lactofermentum
US-10-784-986-24

Query Match 100.0%; Score 620; DB 5; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTMEIFITGLLIGASLLSIGPQNVLVIKQIKREGIAVLVCLISDVFLFIAGTLGV 60
DB 1 MVTMEIFITGLLIGASLLSIGPQNVLVIKQIKREGIAVLVCLISDVFLFIAGTLGV 60
QY 61 DLISNAPIVLDIMRWGIAVILMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPIGVF 120
DB 61 DLISNAPIVLDIMRWGIAVILMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPIGVF 120
QY 121 GGCH 124
DB 121 GGCH 124

RESULT 4
US-10-716-470-10
; Sequence 10, Application US/10716470
; Publication No. US20050003495A1
; GENERAL INFORMATION:
; APPLICANT: Ajinomoto Co., Inc.
; TITLE OF INVENTION: Method For Producing L-Lysine or L-Arginine By Using
; TITLE OF INVENTION: Mechanol Assimilating Bacteria

FILE REFERENCE: 091628
; CURRENT APPLICATION NUMBER: US/10/716,470
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: JP 2002-336340
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Brevibacterium lactofermentum
US-10-716-470-10

Query Match 100.0%; Score 620; DB 5; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTMEIFITGLLIGASLLSIGPQNVLVIKQIKREGIAVLVCLISDVFLFIAGTLGV 60
DB 1 MVTMEIFITGLLIGASLLSIGPQNVLVIKQIKREGIAVLVCLISDVFLFIAGTLGV 60
QY 61 DLISNAPIVLDIMRWGIAVILMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPIGVF 120
DB 61 DLISNAPIVLDIMRWGIAVILMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPIGVF 120
QY 121 GGCH 124
DB 121 GGCH 124

RESULT 5
US-09-738-626-6955
; Sequence 6955, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patentin ver. 3.0
; SEQ ID NO 6955
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6955

Query Match 94.2%; Score 584; DB 3; Length 236;
Best Local Similarity 100.0%; Pred. No. 6.3e-59;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTMEIFITGLLIGASLLSIGPQNVLVIKQIKREGIAVLVCLISDVFLFIAGTLGV 60
DB 1 MVTMEIFITGLLIGASLLSIGPQNVLVIKQIKREGIAVLVCLISDVFLFIAGTLGV 60
QY 61 DLISNAPIVLDIMRWGIAVILMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPIGVF 118
DB 61 DLISNAPIVLDIMRWGIAVILMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPIGVF 118

Db 61 DLSNAAPIVLDIMRWGIAVLLMFAVMAAKDAMTNKVEAPQIIETEPTVPDDTPLG 118

RESULT 6
US-10-166-142-8
; Sequence 8, Application US/10166142
; Publication No. US20030124687A1
; GENERAL INFORMATION:
; APPLICANT: GUNJI, YOSHIYA
; APPLICANT: YASUEDA, HISASHI
; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL
; TITLE OF INVENTION: ASSIMILATING BACTERIUM
; FILE REFERENCE: 223/89US
; CURRENT APPLICATION NUMBER: US/10/166,142
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: JP 2001-1777075
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 8
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Brevibacterium lactofermentum
US-10-166-142-8

Query Match 94.2%; Score 584; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 6.3e-59;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIMEIFITGILLGASLLSIGPQNVLVIKGIRKREGIAVLLVCLISDVFLFIAGTIGV 60
Db 1 WIMEIFITGILLGASLLSIGPQNVLVIKGIRKREGIAVLLVCLISDVFLFIAGTIGV 60

Db 61 DLSNAAPIVLDIMRWGIAVLLMFAVMAAKDAMTNKVEAPQIIETEPTVPDDTPLG 118

RESULT 7
US-10-716-473-8
; Sequence 8, Application US/10716473
; Publication No. US20040142435A1
; GENERAL INFORMATION:
; APPLICANT: Ajinomoto Co. Inc.
; TITLE OF INVENTION: Method for Producing L-Amino Acid Using Methylotroph
; FILE REFERENCE: OP1629
; CURRENT APPLICATION NUMBER: US/10/716,473
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: JP 2002-336346
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Brevibacterium lactofermentum
US-10-716-473-8

Query Match 94.2%; Score 584; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 6.3e-59;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIMEIFITGILLGASLLSIGPQNVLVIKGIRKREGIAVLLVCLISDVFLFIAGTIGV 60
Db 1 WIMEIFITGILLGASLLSIGPQNVLVIKGIRKREGIAVLLVCLISDVFLFIAGTIGV 60

Qy 61 DLSNAAPIVLDIMRWGIAVLLMFAVMAAKDAMTNKVEAPQIIETEPTVPDDTPLG 118
Db 61 DLSNAAPIVLDIMRWGIAVLLMFAVMAAKDAMTNKVEAPQIIETEPTVPDDTPLG 118

RESULT 8
US-10-716-480A-2

; Sequence 2, Application US/10716480A
; Publication No. US20040146974A1
; GENERAL INFORMATION:
; APPLICANT: Ajinomoto Co. Inc.
; TITLE OF INVENTION: Method for Producing L-Amino Acid Using Methylotroph
; FILE REFERENCE: OP1627/US-102
; CURRENT APPLICATION NUMBER: US/10/716,480A
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: JP 2002-336315
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Brevibacterium lactofermentum
US-10-716-480A-2

Query Match 94.2%; Score 584; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 6.3e-59;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIMEIFITGILLGASLLSIGPQNVLVIKGIRKREGIAVLLVCLISDVFLFIAGTIGV 60
Db 1 WIMEIFITGILLGASLLSIGPQNVLVIKGIRKREGIAVLLVCLISDVFLFIAGTIGV 60

Db 61 DLSNAAPIVLDIMRWGIAVLLMFAVMAAKDAMTNKVEAPQIIETEPTVPDDTPLG 118

RESULT 9
US-10-760-283-18
; Sequence 18, Application US/10760283
; Publication No. US20040214296A1
; GENERAL INFORMATION:
; APPLICANT: ASAHARA, Takayuki
; APPLICANT: HIRANO, Seiko
; APPLICANT: YASUEDA, Hisashi
; TITLE OF INVENTION: Method for Producing L-Lysine Using Methanol-utilizing Bacterium
; FILE REFERENCE: OP1631
; CURRENT APPLICATION NUMBER: US/10/760,283
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: JP 2003-20513
; PRIOR FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Brevibacterium lactofermentum
US-10-760-283-18

Query Match 94.2%; Score 584; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 6.3e-59;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIMEIFITGILLGASLLSIGPQNVLVIKGIRKREGIAVLLVCLISDVFLFIAGTIGV 60
Db 1 WIMEIFITGILLGASLLSIGPQNVLVIKGIRKREGIAVLLVCLISDVFLFIAGTIGV 60

Qy 61 DLSNAAPIVLDIMRWGIAVLLMFAVMAAKDAMTNKVEAPQIIETEPTVPDDTPLG 118
Db 61 DLSNAAPIVLDIMRWGIAVLLMFAVMAAKDAMTNKVEAPQIIETEPTVPDDTPLG 118

RESULT 10
US-10-784-986-22
; Sequence 22, Application US/10784986
; Publication No. US20040229311A1
; GENERAL INFORMATION:
; APPLICANT: HIRANO, Seiko
; APPLICANT: YASUEDA, Hisashi

;; TITLE OF INVENTION: Novel lysine decarboxylase gene and method for
;; FILE REFERENCE: US-109
;; CURRENT APPLICATION NUMBER: US/10/784,986
;; CURRENT FILING DATE: 2004-02-25
;; PRIOR APPLICATION NUMBER: JP 2003-47185
;; PRIOR FILING DATE: 2003-02-25
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 22
;; LENGTH: 236
;; TYPE: PRT
;; ORGANISM: Brevibacterium lactofermentum
US-10-784-986-22

Query Match 94.2%; Score 584; DB 5; Length 236;
Best Local Similarity 100.0%; Pred. No. 6.3e-59;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTMEFITGLLGASLLSISGPQNVIVIKGIRREGIIVLVCLISDVFLFIAGTLGV 60
DB 1 MVTMEFITGLLGASLLSISGPQNVIVIKGIRREGIIVLVCLISDVFLFIAGTLGV 60
61 DLSNAPIVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETEPTVPDDTPIG 118
61 DLSNAPIVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETEPTVPDDTPIG 118

RESULT 11
US-10-716-470-8
;; Sequence 8, Application US/10716470
;; Publication No. US20050003495A1
;; GENERAL INFORMATION:
;; APPLICANT: Ajinomoto Co. Inc.
;; TITLE OF INVENTION: Method For Producing L-Lysine or L-Arginine By Using
;; FILE REFERENCE: OPI628
;; CURRENT APPLICATION NUMBER: US/10/716,470
;; CURRENT FILING DATE: 2003-11-20
;; PRIOR APPLICATION NUMBER: JP 2002-336340
;; PRIOR FILING DATE: 2002-11-20
;; NUMBER OF SEQ ID NOS: 14
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 8
;; LENGTH: 236
;; TYPE: PRT
;; ORGANISM: Brevibacterium lactofermentum
US-10-716-470-8

Query Match 94.2%; Score 584; DB 5; Length 236;
Best Local Similarity 100.0%; Pred. No. 6.3e-59;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTMEFITGLLGASLLSISGPQNVIVIKGIRREGIIVLVCLISDVFLFIAGTLGV 60
DB 1 MVTMEFITGLLGASLLSISGPQNVIVIKGIRREGIIVLVCLISDVFLFIAGTLGV 60
QY 61 DLSNAPIVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETEPTVPDDTPIG 118
DB 61 DLSNAPIVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETEPTVPDDTPIG 118

RESULT 12
US-09-746-660A-52
;; Sequence 52, Application US/09746660A
;; Publication No. US20030049804A1
;; GENERAL INFORMATION:
;; APPLICANT: Pompejus, Markus
;; APPLICANT: Krieger, Burkhard
;; APPLICANT: Schroder, Hartwig
;; APPLICANT: Zelder, Oskar
;; APPLICANT: Haberhauer, Gregor
;; APPLICANT: Klm, Jun-Mon

;; APPLICANT: Lee, Heung-Schick
;; APPLICANT: Hwang, Byung-Joon
;; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
;; FILE REFERENCE: BGI-121CP2
;; CURRENT APPLICATION NUMBER: US/09/746,660A
;; CURRENT FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 09/606740
;; PRIOR FILING DATE: 2000-06-23
;; PRIOR APPLICATION NUMBER: 09/603124
;; PRIOR FILING DATE: 2000-06-23
;; PRIOR APPLICATION NUMBER: 60/141031
;; PRIOR FILING DATE: 1999-06-25
;; PRIOR APPLICATION NUMBER: 60/142101
;; PRIOR FILING DATE: 1999-07-02
;; PRIOR APPLICATION NUMBER: 60/148613
;; PRIOR FILING DATE: 1999-08-12
;; PRIOR APPLICATION NUMBER: 60/187970
;; PRIOR FILING DATE: 2000-03-09
;; PRIOR APPLICATION NUMBER: DE 19931420.9
;; PRIOR FILING DATE: 1999-07-08
;; NUMBER OF SEQ ID NOS: 125
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 52
;; LENGTH: 233
;; TYPE: PRT
;; ORGANISM: Corynebacterium glutamicum
US-09-746-660A-52

Query Match 92.1%; Score 571; DB 3; Length 233;
Best Local Similarity 100.0%; Pred. No. 2e-57;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MEIFITGLLGASLLSISGPQNVIVIKGIRREGIIVLVCLISDVFLFIAGTLGV 63
DB 1 MEIFITGLLGASLLSISGPQNVIVIKGIRREGIIVLVCLISDVFLFIAGTLGV 60
QY 64 SNAPIVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETEPTVPDDTPIG 118
DB 61 SNAPIVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETEPTVPDDTPIG 115

RESULT 13
US-10-196-232-25
;; Sequence 25, Application US/10196232
;; Publication No. US20030113899A1
;; GENERAL INFORMATION:
;; APPLICANT: YAMAGUCHI, MIKIKO
;; APPLICANT: ITO, HISAO
;; APPLICANT: GUNJI, YOSHIA
;; APPLICANT: YASUEDA, HISASHI
;; TITLE OF INVENTION: METHOD FOR PRODUCING L-ARGININE
;; FILE REFERENCE: 225391US0
;; CURRENT APPLICATION NUMBER: US/10/196,232
;; CURRENT FILING DATE: 2002-07-17
;; PRIOR APPLICATION NUMBER: JP 2001-224586
;; PRIOR FILING DATE: 2001-07-25
;; NUMBER OF SEQ ID NOS: 35
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 25
;; LENGTH: 233
;; TYPE: PRT
;; ORGANISM: Corynebacterium glutamicum
US-10-196-232-25

Query Match 92.1%; Score 571; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 2e-57;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MEIFITGLLGASLLSISGPQNVIVIKGIRREGIIVLVCLISDVFLFIAGTLGV 63
DB 1 MEIFITGLLGASLLSISGPQNVIVIKGIRREGIIVLVCLISDVFLFIAGTLGV 60

QY 64 SNAAPVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPLG 118
DB 61 SNAAPVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPLG 115

RESULT 14
US-10-858-730-234
Sequence 234, Application US/10858730
Publication No. US2005025568A1
GENERAL INFORMATION:
APPLICANT: Bailey, Richard B.
APPLICANT: Blomquist, Paul
APPLICANT: Doten, Reed
APPLICANT: Driggers, Edward M.
APPLICANT: Madden, Kevin T.
APPLICANT: O'Leary, Jessica
APPLICANT: O'Toole, George
APPLICANT: Trueheart, Joshua
APPLICANT: Walbridge, Michael J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
FILE OF INVENTION: PRODUCTION
FILE REFERENCE: 14184-030001
CURRENT APPLICATION NUMBER: US/10/858,730
CURRENT FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/475,000
PRIOR FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: US 60/551,860
PRIOR FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 364
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 234
LENGTH: 233
TYPE: PRT
ORGANISM: Coryne-bacterium glutamicum
US-10-858-730-234

Query Match 92.1%; Score 571; DB 5; Length 233;
Best Local Similarity 100.0%; Pred. No. 2e-57;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MEIIFITGLLGASLSLISIPQNVLVTKQIKREGIAVLLVCLISDVFLFIAGTLGVDLL 63
DB 1 MEIIFITGLLGASLSLISIPQNVLVTKQIKREGIAVLLVCLISDVFLFIAGTLGVDLL 60

QY 64 SNAAPVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPLG 118
DB 61 SNAAPVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPLG 115

RESULT 15
US-11-055-822-54
Sequence 54, Application US/11055822
Publication No. US20050260707A1
GENERAL INFORMATION:
APPLICANT: Pompeius, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
FILE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121PCN
CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/148,613
PRIOR FILING DATE: 1999-08-12

PRIOR APPLICATION NUMBER: 60/187,970
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: DE 19930476.9
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931415.2
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931418.7
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR FILING DATE: 1999-07-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 54
LENGTH: 233
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-11-055-822-54

Query Match 92.1%; Score 571; DB 6; Length 233;
Best Local Similarity 100.0%; Pred. No. 2e-57;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MEIIFITGLLGASLSLISIPQNVLVTKQIKREGIAVLLVCLISDVFLFIAGTLGVDLL 63
DB 1 MEIIFITGLLGASLSLISIPQNVLVTKQIKREGIAVLLVCLISDVFLFIAGTLGVDLL 60

QY 64 SNAAPVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPLG 118
DB 61 SNAAPVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPLG 115

Search completed: July 19, 2006, 00:46:18
Job time : 189 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2006, 00:25:46 ; Search time 40 Seconds

(without alignments)
298.272 Million cell updates/sec

Title: US-10-716-470-10

Perfect score: 620

Sequence: 1 MVMEIFITGLLIGASLLS.....ETEPTVPDDPLGFGGGR 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	213	34.4	211	1	OQEC5A
2	210	33.9	211	2	E85948
3	210	33.9	211	2	B91103
4	205	33.1	211	2	AH0874
5	199.5	32.2	205	2	AG0112
6	193.5	31.2	202	2	C97472
7	193.5	31.2	202	2	AG2690
8	172.5	27.8	200	2	D83100
9	170	27.4	199	2	H70756
10	169	27.3	204	2	AD3411
11	154	24.8	201	2	C70744
12	135	21.8	211	2	S57940
13	116	18.7	211	2	B82318
14	109	17.6	210	2	D84016
15	107	17.3	210	2	E87252
16	105	16.9	220	2	D69638
17	104	16.8	205	2	B89854
18	99	16.0	212	2	AD0714
19	94.5	15.2	235	2	AD2904
20	94.5	15.2	235	2	F97679
21	94	15.2	216	2	AH3703
22	92	14.8	200	2	G83703
23	91	14.7	208	2	G84086
24	91	14.7	210	2	F64609
25	88.5	14.3	212	2	B71906
26	87	14.0	195	2	F69490
27	86	13.9	197	2	AF0830
28	86	13.9	207	2	B83703

30	86	13.9	213	2	F83444	hypothetical prote
31	85.5	13.8	222	2	F82353	conserved hypochet
32	84.5	13.6	209	2	E82388	conserved hypochet
33	84	13.5	210	2	AC2982	RhtB family transp
34	83.5	13.5	278	2	E98301	hypothetical prote
35	82.5	13.5	218	2	A96009	probable amino aci
36	82.5	13.3	212	2	C90942	hypothetical prote
37	82.5	13.3	212	2	G85790	hypothetical prote
38	82.5	13.3	213	2	E97789	hypothetical prote
39	80	12.9	208	1	B69066	conserved hypochet
40	80	12.9	343	2	G87419	cytochrome c oxida
41	80	12.9	510	2	G71365	probable carnitine
42	79.5	12.8	210	2	G83082	hypothetical prote
43	79.5	12.8	442	2	T24196	hypothetical prote
44	79	12.7	222	2	E87264	efflux protein, Ly
45	78	12.6	212	2	AB3270	threonine efflux p

ALIGNMENTS

RESULT 1

OQEC5A hypothetical 23K protein (sbm-fba intergenic region) - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C:Date: 31-Dec-1990 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004

C:Accession: B65077; S04736

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; (

A.: Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MWID:97426617; PMID:9278503

A:Accession: B65077

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-211 <BLAT>

A:Cross-references: UNIPROT:P11667; UNIPARC:UPI0000033982; GB:AE000375; GB:U00096; NID:

A:Experimental source: strain K-12, substrain MG1655

R:Alfunder, P.R.; Perham, R.N.

Mol. Microbiol. 3, 723-732, 1989

A:Title: Identification, molecular cloning and sequence analysis of a gene cluster enc

hyde 3-phosphate dehydrogenase of Escherichia coli.

A:Reference number: S04730; MWID:89313302; PMID:2546007

A:Accession: S04736

A:Molecule type: DNA

A:Residues: 15-211 <ALF>

A:Cross-references: UNIPARC:UPI000016F130; EMBL:X14436; NID:941417; PIDD:CAA32607.1; P1

A:Gene: Y9GA

A:Map position: 63 min

C:superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)

Query Match

Best Local Similarity 34.4%; Score 213; DB 1; Length 211;

Matches 40; Conservative 21; Mismatches 32; Indels 0; Gaps 0;

QY

7 FITGILGASLLSISGPGQVAVIKQIKREGLAVLVLCISDVFFINGTIGVLLSNA 66

5 YFQGLALGAMTLPISGPQAFVFNQGIKQYHIMTALCAISDLVICGIRGSGALLMQ 64

DB

67 APIVDIMRGGIAVLTFWVAAMADMTNRYE 99

65 SPMLALVTWGVAFVFLWVGFAFTANSSNIE 97

QY

DB

QY

DB

QY

DB

RESULT 2
hypothetical protein Y9GA [imported] - Escherichia coli (strain O157:H7, substrain EDJ9

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C:Accession: B65948

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayne

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamoustis, K.; Apodaca

Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E85948
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-211 <STO>
A:Cross-references: UNIPROT:Q8XD10; UNIPARC:UPI0000165916; GB:AE005174; NID:g12517455; F
A:Experimental source: strain O157:H7, substrain EDL933
A:Gene: Y99A
C:Superfamily: *Escherichia coli* hypothetical 23K protein (sbm-fba intergenic region)
Query Match 33.9%; Score 210; DB 2; Length 211;
Best Local Similarity 35.1%; Pred. No. 1.3e-13;
Matches 47; Conservative 27; Mismatches 42; Indels 18; Gaps 3;
OY 7 FITGILLGASLLISIGPQNVLVIRKQIREGLIAVLVCLISDVFLFIAGTLGVDLSNA 66
Db 5 YFGGLAAGAAWILPLGPQNAFVNMGIROVHIMIALCALSDVLICAGIFGGSALLMO 64
OY 67 APIVLDIRKGGIAYLLMFVMAAKDAMTKVE--APQIIIE-----TEPT 110
Db 65 SPWLLALVTWGVFLWYGFAGFKTAMSSNIELASAEVLKQGRWKIATMLAVTMLNPH 124
OY 111 VPDDT--PLGVFGG 122
Db 125 VYLDTPFVVLGSLGG 138
RESULT 3
B91103
hypothetical protein EC83794 [imported] - *Escherichia coli* (strain O157:H7, substrain R1
C:Species: *Escherichia coli*
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: B91103
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: B91103
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-211 <HAV>
A:Cross-references: UNIPROT:Q8XD10; UNIPARC:UPI00000D03F2; GB:BA000007; PIDN:BA837217.1;
A:Experimental source: strain O157:H7, substrain R1MD 050952
A:Gene: EC83794
C:Superfamily: *Escherichia coli* hypothetical 23K protein (sbm-fba intergenic region)
Query Match 33.9%; Score 210; DB 2; Length 211;
Best Local Similarity 35.1%; Pred. No. 1.3e-13;
Matches 47; Conservative 27; Mismatches 42; Indels 18; Gaps 3;
OY 7 FITGILLGASLLISIGPQNVLVIRKQIREGLIAVLVCLISDVFLFIAGTLGVDLSNA 66
Db 5 YFGGLAAGAAWILPLGPQNAFVNMGIROVHIMIALCALSDVLICAGIFGGSALLMO 64
OY 67 APIVLDIRKGGIAYLLMFVMAAKDAMTKVE--APQIIIE-----TEPT 110
Db 65 SPWLLALVTWGVFLWYGFAGFKTAMSSNIELASAEVLKQGRWKIATMLAVTMLNPH 124
OY 111 VPDDT--PLGVFGG 122
Db 125 VYLDTPFVVLGSLGG 138
RESULT 4
AH0874
probable membrane transport protein STY3222 [imported] - *Salmonella enterica* subsp. *ente*
C:Species: *Salmonella enterica* subsp. *enterica* serovar *Typh*
A:Note: this species has also been called *Salmonella typh*

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AH0874
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* sero
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH0874
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-211 <PAR>
A:Cross-references: UNIPARC:UPI000005A426; GB:AL513382; PIDN:CAD02896.1; PID:g16504149;
A:Gene: STY3222
C:Superfamily: *Escherichia coli* hypothetical 23K protein (sbm-fba intergenic region)
Query Match 33.1%; Score 205; DB 2; Length 211;
Best Local Similarity 38.1%; Pred. No. 4e-13;
Matches 37; Conservative 26; Mismatches 34; Indels 0; Gaps 0;
OY 3 IMEFTIGLLGASLLISIGPQNVLVIRKQIREGLIAVLVCLISDVFLFIAGTLGVDL 62
Db 1 MISYFQGVALLGAAWILPLGPQNAFVNMGIROVHIMIALCALSDVLISAGIFGSA 60
OY 63 LSNAPIVLDIRKGGIAYLLMFVMAAKDAMTKVE 99
Db 61 LMQSPWLLALVTWGVFLWYGFAGFKTAMSSNLE 97
RESULT 5
AG0112
probable lysE type translocator YPO0918 [imported] - *Yersinia pestis* (strain CO92)
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AG0112
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titchall, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
H, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AG0112
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-205 <KUR>
A:Cross-references: UNIPROT:Q8ZHN6; UNIPARC:UPI00000DC792; GB:AL590842; PIDN:CAC89762.1;
A:Gene: YPO0918
C:Superfamily: *Escherichia coli* hypothetical 23K protein (sbm-fba intergenic region)
Query Match 32.2%; Score 199.5; DB 2; Length 205;
Best Local Similarity 38.5%; Pred. No. 1.4e-12;
Matches 35; Conservative 27; Mismatches 26; Indels 3; Gaps 1;
OY 3 IMEFTIGLLGASLLISIGPQNVLVIRKQIREGLIAVLVCLISDVFLFIAGTLGVDL 62
Db 1 MLAVLHGFILSLAAMILPLGPQNAFVNMGIROVHIMIALCALSDVLICAGIFGSA 60
OY 63 LSNAPIVLDIRKGGIAYLLMF--AVMAA 90
Db 61 LLSRSPILLALVTWGVAFLLWYGMGLWMA 91
RESULT 6
C97472
probable membrane transport protein. (AL357613) [imported] - *Agrobacterium tumefaciens* (C
C:Species: *Agrobacterium tumefaciens*
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: C97472
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*
A/Reference number: A97359; MUID:21608551; PMID:11743194
A/Accession: C97472
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-202 <KUR>
A/Cross-references: UNIPROT:Q8UGV8; UNIPARC:UPI000000D199F; GB:AE007869; PIND:AAK6732.1
C/Genetics:
A/Gene: AGR_C_1690
A/Map position: circular chromosome
C/Superfamily: Escherichia coli hypothetical 23k protein (sbm-fba intergenic region)

Query Match 31.2%; Score 193.5; DB 2; Length 202;
Best Local Similarity 36.1%; Pred. No. 5.4e-12;
Matches 39; Conservative 22; Mismatches 46; Indels 1; Gaps 1;

QY 4 MEFTTGLGASLLSIGPQNVLVKQIKREGIAVLVCLISDFLFIAGTLGVDL 63
DB 3 IQFTFTGLTGLSLIVAIGQNAFVLKQGLARSHVFAVCATCAISDALLIMVGFGFORI 62

QY 64 SNAAPVLDIRMGIAVLIMFAVMAKADMTNKVEAPQIIEETPTV 111
DB 63 SAIMPALDIRMYAGAAFLIMYGAKSLYSALRSS-EVLSVAERREASL 109

RESULT 7
AG2690
lysE family transporter lysE [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
C/Species: *Agrobacterium tumefaciens*
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
A/Accession: AG2690
R/Wood, D.W.; Seubald, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moe, L.; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A>Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AG2690
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-202 <KUR>
A/Cross-references: UNIPROT:Q8UGV8; UNIPARC:UPI000000D199F; GB:AE006688; PIND:ALL41941.1
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Gene: lysE
A/Map position: circular chromosome
C/Superfamily: Escherichia coli hypothetical 23k protein (sbm-fba intergenic region)

Query Match 31.2%; Score 193.5; DB 2; Length 202;
Best Local Similarity 36.1%; Pred. No. 5.4e-12;
Matches 39; Conservative 22; Mismatches 46; Indels 1; Gaps 1;

QY 4 MEFTTGLGASLLSIGPQNVLVKQIKREGIAVLVCLISDFLFIAGTLGVDL 63
DB 3 IQFTFTGLTGLSLIVAIGQNAFVLKQGLARSHVFAVCATCAISDALLIMVGFGFORI 62

QY 64 SNAAPVLDIRMGIAVLIMFAVMAKADMTNKVEAPQIIEETPTV 111
DB 63 SAIMPALDIRMYAGAAFLIMYGAKSLYSALRSS-EVLSVAERREASL 109

RESULT 8
DB3100
Probable transporter PA4365 [imported] - *Pseudomonas aeruginosa* (strain PAO1)
C/Species: *Pseudomonas aeruginosa*
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
A/Accession: DB3100
R/Stover, C.K.; Pham, X.Q.; Edwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kass, A.; Lapidis, K.; Lam, S.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000
A>Title: Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic pathogen
A/Reference number: AB2950; MUID:20437337; PMID:10984043
A/Accession: DB3100
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-200 <STO>
A/Cross-references: UNIPROT:Q9HW36; UNIPARC:UPI000000CCE3; GB:AE004852; GB:AE004091; N
C/Genetics:
A/Gene: PA4365
C/Superfamily: Escherichia coli hypothetical 23k protein (sbm-fba intergenic region)

Query Match 27.8%; Score 172.5; DB 2; Length 200;
Best Local Similarity 35.7%; Pred. No. 6.6e-10;
Matches 35; Conservative 20; Mismatches 38; Indels 5; Gaps 1;

QY 7 FTGTLGASLLSIGPQNVLVKQIKREGIAVLVCLISDFLFIAGTLGVDL 66
DB 5 YLNGILVAAGLITIAIGQNAFVLQSLRRHHSVALCVPCDAVLSLVGFLAKLLE 64

QY 67 APIVLDIRMGIAVLIMFAVMAKADMTNKVE 99
DB 65 NPTLAIARWGIAFLTWGLKALPRLRBDALGNAE 102

RESULT 9
H70756
hypothetical protein RV1986 - *Mycobacterium tuberculosis* (strain H37Rv)
C/Species: *Mycobacterium tuberculosis*
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
A/Accession: H70756
R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holtroyd, R.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A/Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
A>Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A/Reference number: A70500; MUID:9825987; PMID:9634230
A/Accession: H70756
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-199 <COL>
A/Cross-references: UNIPROT:Q10871; UNIPARC:UPI000011B4E7; GB:274025; GB:AL123456; NID:
A/Experimental source: strain H37Rv
C/Genetics:
A/Gene: RV1986
C/Superfamily: Escherichia coli hypothetical 23k protein (sbm-fba intergenic region)

Query Match 27.4%; Score 170; DB 2; Length 199;
Best Local Similarity 37.2%; Pred. No. 1.2e-09;
Matches 32; Conservative 24; Mismatches 30; Indels 0; Gaps 0;

QY 8 ITGTLGASLLSIGPQNVLVKQIKREGIAVLVCLISDFLFIAGTLGVDL 67
DB 6 VVGFLACFLITIAIGQNAFVLQSLRRHHSVALCVPCDAVLSLVGFLAKLLE 65

QY 68 PIVLDIRMGIAVLIMFAVMAKAD 93
DB 66 PRALNVKFGGAFLIGYGLAARRA 91

RESULT 10
AD3411
transporter, lysE family BMEI1274 [imported] - *Brucella melitensis* (strain 16M)
C/Species: *Brucella melitensis*
C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
A/Accession: AD3411
R/Belvacchio, V.G.; Kaparakis, V.; Radkar, R.J.; Patra, G.; Mui, C.; Lo, T.; Ivanova, A.; Masur, M.; Goldstein, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Lete Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A>Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
A/Reference number: AD3252; PMID:11756688

A:Accession: AD3411
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-204 <KOR>
 A:Cross-references: UNIPROT:Q8YG87; UNIPARC:UPI0000057EE3; GB:AE008917; PIDN:AAL52455.1;
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEL1274
 A:Map position: 1
 C:Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)

Query Match 27.3%; Score 169; DB 2; Length 204;
 Best Local Similarity 35.4%; Pred. No. 1.5e-09;
 Matches 34; Conservative 24; Mismatches 36; Indels 2; Gaps 1;

QY 8 ITGLLGASLLSIPQNVLVKQIKREGIAVLVCLISDVFLFIAGTGVLDLSNAA 67
 Db 6 LSGFLGASLLIAIGQNAFLRQGLRQHVFILCLISDALISAGVAGLTLLAQS 65

QY 68 PIVLDIRMGIAVLVFAVMAAKDAMTKVEAPQI 103
 Db 66 PKLIAFVTLGAAFLFWYASVAFRRAF--HPEAMQV 99

RESULT 11
 C70744
 hypothetical protein Rv0488 - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: C70744
 R:Coile, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
 A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9631230
 A:Accession: C70744
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-201 <COL>
 A:Cross-references: UNIPROT:Q1154; UNIPARC:UPI0000139897; GB:Z77162; GB:AL123456; NID:5
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: Rv0488
 C:Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)

Query Match 24.8%; Score 154; DB 2; Length 201;
 Best Local Similarity 39.7%; Pred. No. 4.6e-08;
 Matches 31; Conservative 23; Mismatches 24; Indels 0; Gaps 0;

QY 16 SLLSIPQNVLVKQIKREGIAVLVCLISDVFLFIAGTGVLDLSNAAPIVLDIMR 75
 Db 3 TLKVAIPQNAFVLRQGIIRREYLVIVALCGIADGALIAVGGAFLIHAHPMTLVAR 62

QY 76 WGGIAYLLMFVMAKXA 93
 Db 63 FCGAFLIGYALLAARNA 80

RESULT 12
 S57940
 YggA protein homolog - Aeromonas hydrophila
 C:Species: Aeromonas hydrophila
 C>Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999
 C:Accession: S57940
 R:Swift, S.; Fish, L.; Williams, P.; Stewart, G.S.A.B.
 submitted to the EMBL Data Library, July 1995
 A:Reference number: S57938
 A:Accession: S57940
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-211 <SWI>

A:Cross-references: UNIPARC:UPI000016E4DC; EMBL:X89469; NID:G899143; PIDN:CA61655.1; P:
 Query Match 21.8%; Score 135; DB 2; Length 211;
 Best Local Similarity 29.3%; Pred. No. 3.3e-06;
 Matches 27; Conservative 22; Mismatches 39; Indels 4; Gaps 1;

QY 17 LLSISIPQNVLVKQIKREGIAVLVCLISDVFLFIAGTGVLDLSNAAPIVLDIMRW 76
 Db 1 MIIPIGQNAFVLSRGIRHRHHLLTATLCCLDVILIGIVFGGANLLASPIGLALLTW 60

QY 77 GGIAYLLMFVMAKAMTKN---VEAPQII 104
 Db 61 GGVILFGMFGIRSLRSARMGAKLADSPQLM 92

RESULT 13
 B82318
 Lyse/YggA family protein VCO481 [imported] - Vibrio cholerae (strain N16961 serogroup O:
 C:Species: Vibrio cholerae
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: B82318
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, J. 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: B82318
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-211 <HEI>
 A:Cross-references: UNIPROT:Q9KDM4; UNIPARC:UPI00000C2CE3; GB:AE004134; GB:AE003852; NII
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VCO481
 A:Map position: 1
 C:Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)

Query Match 18.7%; Score 116; DB 2; Length 211;
 Best Local Similarity 26.7%; Pred. No. 0.0003;
 Matches 31; Conservative 21; Mismatches 60; Indels 4; Gaps 1;

QY 6 IFITGLLAGSLLSIPQNVLVKQIKREGIAVLVCLISDVFLFIAGTGVLDLSN 65
 Db 5 ILLGSLGATMIIPGQNAFVLRQGIIRHRHHLLTAAATCGVDMFITIGTGGGLIS 64

QY 66 AAPIVDIRMGIAVLVFAVMAAKDAMTKNVEAPQIIEETEPVDDTPIGVFG 121
 Db 65 QNTSLIIGVTLGILFLFCGVGFLSLRAL---KPROASESTANPMAGRAKAVIFG 116

RESULT 14
 D84016
 hypothetical protein BH2932 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C:Accession: D84016
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: D84016
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-210 <STO>
 A:Cross-references: UNIPROT:Q9K8S1; UNIPARC:UPI00000C4058; GB:AP001517; GB:BA000004; NII
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH2932
 C:Superfamily: hypothetical protein b1798

Query Match 17.6%; Score 109; DB 2; Length 210;
 Best Local Similarity 32.1%; Pred. No. 0.0015;

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2006, 00:22:17 / Search time 298 Seconds

(without alignments)
384.906 Million cell updates/sec

Title: US-10-716-470-10

Perfect score: 620
Sequence: 1 MYIMEIFITGLLIGASLLLS.....EETEPVDDPTPLGVGGGH 124

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Uniprot_7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	607	97.9	121	2	Q4H475_CORGL
2	571	92.1	233	1	LYSE_CORGL
3	571	92.1	233	2	Q4H476_CORGL
4	389.5	62.8	228	1	LYSE_CORGL
5	271	43.7	228	1	LYSE_CORGL
6	214	34.5	211	1	ARGO_ECOLI
7	214	34.5	211	1	Q32BY3_SHIDS
8	213	34.4	211	1	ARGO_ECOLI
9	213	34.4	211	2	Q2M9R9_ECOLI
10	212	34.2	211	1	Q3YXU9_SHISS
11	210	33.9	211	1	ARGO_ECOLI
12	210	33.9	211	1	ARGO_SHIFL
13	207	33.4	211	2	Q3LW12_SHIBS
14	205	33.1	211	1	ARGO_SALTI
15	204	32.9	211	1	ARGO_SALCH
16	204	32.9	211	1	ARGO_SALTY
17	200	32.3	211	1	ARGO_SALPA
18	199.5	32.2	205	1	ARGO_YERPE
19	199.5	32.2	205	1	ARGO_YERPS
20	198	31.9	204	1	ARGO_YERPS
21	194	31.3	203	2	Q5LUH5_SILPO
22	193.5	31.2	202	2	Q8UV8_AGR5
23	191.5	30.9	196	2	Q4NL65_GMTCC
24	189	30.5	202	2	Q3H1Y4_GACTO
25	189	30.5	202	2	Q2K7B0_RHET
26	187.5	30.2	203	2	Q4O6B0_RHOB
27	187	30.2	200	2	Q4ZP34_PSEU2
28	186	30.0	221	2	Q4OYM9_KINRA
29	185	29.8	203	2	Q2RMA4_RHORB
30	183	29.5	200	2	Q48EJ9_PSE14
31	183	29.5	206	2	Q7ZE15_DESVH

ALIGNMENTS

32	180	29.0	200	2	Q87X28_PSESM	Q87X28 pseudomonas
33	179	28.9	202	2	Q8XXT9_RALSO	Q8XXT9 ralsconia s
34	178	28.7	214	2	Q39T4_BUR83	Q39T4 burkholderi
35	177	28.5	212	2	Q8Y2F1_RALSO	Q8Y2F1 ralsconia s
36	176	28.4	207	1	ARGO_PFOUL	Q7N183 photorhabdu
37	175	28.2	200	2	Q4K777_PSEPS	Q4K770 pseudomonas
38	174	28.1	204	2	Q227Y0_9GAMM	Q227Y0 shewanella
39	174	28.1	204	2	Q35S87_9GAMM	Q35S87 shewanella
40	174	28.1	204	2	Q36DP7_9GAMM	Q36DP7 shewanella
41	174	28.1	211	2	Q7N1Y0_CHRYO	Q7N1Y0 chromobacte
42	173	27.9	213	2	Q2X624_9GAMM	Q2X624 shewanella
43	173	27.9	213	2	Q2ZLZ4_SHEPU	Q2ZLZ4 shewanella
44	172.5	27.8	200	2	Q9HW36_PSESE	Q9HW36 pseudomonas
45	172	27.7	199	2	Q3PH95_PARDE	Q3PH95 paracoccus

RESULT 1

Q4H475_CORGL PRELIMINARY; PRT; 121 AA.

AC Q4H475; 30-AUG-2005, integrated into UniProtKB/TrEMBL.

DT 30-AUG-2005, sequence version 1.

DT 07-FEB-2006, entry version 2.

DE Mutant lysine exporter protein.

GN Name=Lyse24;

OS Corynebacterium glutamicum (Brevibacterium flavum).

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.

OX NCBI_Taxid=1718;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 13669;

RA Gunji Y., Sugimoto S., Yasueda H.;

RT "Functional expression of mutant lyse gene for production of L-lysine

in Methylophilus methylotrophus.";

RL Submitted (JAN-2005) to the EMBL/Genbank/DBJ databases.

CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms

CC Distributed under the Creative Commons Attribution-NonCommercial license

CC EMBL; AB199585; BAE07189.1; -; Genomic DNA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005293; P:lysine permease activity; IEA.

DR GO; GO:0006865; P:amino acid transport; IEA.

DR InterPro; IPR001123; Lyse.

DR Pfam; PF01810; Lyse; 1.

SQ SEQUENCE 121 AA; 12844 MW; 379986812602DA60 CRC64;

Query Match 97.9%; Score 607; DB 2; Length 121;

Best Local Similarity 100.0%; Pred. No. 6.2e-50; Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	4	MEIFITGLLIGASLLSIGPQVNLTKQIKREGIAVLVLCIDVFLFAGTGVDL	63
DB	1	MEIFITGLLIGASLLSIGPQVNLTKQIKREGIAVLVLCIDVFLFAGTGVDL	60
QY	64	SNAPDIVIDIRMGIAVLMPVAAADMTNKVEAOIIEETPTVDDPTPLGVGGG	123
DB	61	SNAPDIVIDIRMGIAVLMPVAAADMTNKVEAOIIEETPTVDDPTPLGVGGG	120
QY	124	H 124	
DB	121	H 121	

RESULT 2

LYSE_CORGL STANDARD; PRT; 233 AA.

ID P94633; 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.

DT 14-AUG-2001, sequence version 2.
 DT 07-MAR-2006, entry version 38.
 DE lysine exporter protein.
 GN Name=lysE; OrderedLocustNames=Cg11262, cg1424;
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
 NCBI_TaxID=1718;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND FUNCTION.
 RC STRAIN=R127;
 RX MEDLINE=97126810; PubMed=8971704;
 RA Vrijic M.M., Sahn H., Eggeling L.;
 RT "A new type of transporter with a new type of cellular function: L-lysine export from Corynebacterium glutamicum.";
 RL Mol. Microbiol. 22:815-826(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
 RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RX MEDLINE=22830012; PubMed=1294826; DOI=10.1016/S0168-1656(03)00154-8;
 RA Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M., Burkowski A., Duesch N., Eggeling L., Eikmanns B.J., Gaigalat L., Goessens A., Hartmann M., Hutmacher K., Kraemer R., Linke B., McHardy A.C., Meyer F., Moeckel B., Pfeifferle W., Puelhner A., Ray D.A., Rueckert C., Rupp O., Sahn H., Wendisch V.F., Wiegand I., Tauch A.;
 RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins.";
 RL J. Biotechnol. 104:5-25(2003).
 CC -1- FUNCTION: Involved in the efflux of excess of L-lysine. This is necessary to control the intracellular L-lysine level.
 CC -1- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass membrane protein.
 CC -1- SIMILARITY: Belongs to the lysE/argo transporter (TC 2.A.75) family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License

DR EMBL, X96471, CA65324.2, -, Genomic DNA.
 DR EMBL, BA000036, BAB9865.1, -, ALT_INIT; Genomic DNA.
 DR EMBL, BX927151, CAP19965.1, -, Genomic DNA.
 DR GenomeReviews: BX927147 GR; cg1424.
 DR GenomeReviews: BA000036 GR; cg11262.
 DR InterPro: IPR004777; Lys exporter.
 DR InterPro: IPR001123; LysE.
 DR Pfam: PF01810; LysE; 1.
 DR TIGRFAMs: TIGR00948; 2a75; 1.
 KM Complete proteome; Inner membrane; Membrane; Transmembrane; Transport.
 FT CHAIN 1 233 /FTid=PRO_0000204157.
 FT TRANSMEM 3 23 Potential.
 FT TRANSMEM 35 55 Potential.
 FT TRANSMEM 66 86 Potential.
 FT TRANSMEM 144 164 Potential.
 FT TRANSMEM 177 197 Potential.
 FT TRANSMEM 213 233 Potential.
 SQ SEQUENCE 233 AA; 25082 MW; FSPD9B1ACAD11D13 CRC64;

Query Match 92.1%; Score 571; DB 1; Length 233;
 Best Local Similarity 100.0%; Pred. No. 3.2e-46;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MEFFITGLLGLASLLSISGPNVIVIKQIKREGILAVLVCLISDFLFIAGTGVDDL 63
 DB 1 MEFFITGLLGLASLLSISGPNVIVIKQIKREGILAVLVCLISDFLFIAGTGVDDL 60

OY 64 SNAPIVLDIMRWGIAVLLMFVMAAKDAMTKVAPQIIETEPTVPDPTPLG 118
 DB 61 SNAPIVLDIMRWGIAVLLMFVMAAKDAMTKVAPQIIETEPTVPDPTPLG 115

RESULT 3
 ID Q4H476 CORGL PRELIMINARY; PRT; 233 AA.
 AC Q4H476 CORGL
 DT 30-AUG-2005, integrated into UniProtKB/TrEMBL.
 DT 30-AUG-2005, sequence version 1.
 DT 07-FEB-2006, entry version 2.
 DE lysine exporter protein.
 GN Name=lysE;
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
 NCBI_TaxID=1718;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 13869;
 RA Gunji Y., Sugimoto S., Yasueda H.;
 RT "Functional expression of mutant lysE gene for production of L-lysine in *Methylophilus methylotrophus*.";
 RL Submitted (JAN-2005) to the EMBL/Genbank/DBJ databases.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License

DR EMBL, AB195984, BAB07188.1, -, Genomic DNA.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0015020; C: membrane; IEA.
 DR GO: GO:0005293; F: lysine permease activity; IEA.
 DR GO: GO:0006865; P: amino acid transport; IEA.
 DR InterPro: IPR004777; Lys exporter.
 DR InterPro: IPR001123; LysE.
 DR Pfam: PF01810; LysE; 1.
 DR TIGRFAMs: TIGR00948; 2a75; 1.
 SQ SEQUENCE 233 AA; 25082 MW; FSPD9B1ACAD11D13 CRC64;

Query Match 92.1%; Score 571; DB 2; Length 233;
 Best Local Similarity 100.0%; Pred. No. 3.2e-46;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MEFFITGLLGLASLLSISGPNVIVIKQIKREGILAVLVCLISDFLFIAGTGVDDL 63
 DB 1 MEFFITGLLGLASLLSISGPNVIVIKQIKREGILAVLVCLISDFLFIAGTGVDDL 60

OY 64 SNAPIVLDIMRWGIAVLLMFVMAAKDAMTKVAPQIIETEPTVPDPTPLG 118
 DB 61 SNAPIVLDIMRWGIAVLLMFVMAAKDAMTKVAPQIIETEPTVPDPTPLG 115

RESULT 4
 ID LYS_E COREF STANDARD; PRT; 228 AA.
 AC Q8R0M4;
 DT 01-NOV-2002, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-2002, sequence version 2.
 DT 07-MAR-2006, entry version 24.
 DE lysine exporter protein.
 GN Name=lysE; OrderedLocustNames=CE1357;
 OS Corynebacterium efficiens.
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
 NCBI_TaxID=152794;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
 RA Iwata H., Kimura E., Kawahara Y., Sugimoto S.;
 RT "lysE, lysE of Corynebacterium efficiens.";
 RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.

```

RN      [2]
RP      NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC      STRAIN=YS-314 / AJ12310 / DSM 44549 / JCM 11189;
RX      MEDLINE=22723752; PubMed=12840036; DOI=10.1101/5F.1285603;
RA      Nishio Y., Nakamura Y., Kawarayashi Y., Usuda Y., Kimura E.,
RA      Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA      Gojobori T.;
RT      "Comparative complete genome sequence analysis of the amino acid
RT      replacements responsible for the thermostability of Corynebacterium
RT      efficiens."
RL      Genome Res. 13:1572-1579(2003).
CC      -1- FUNCTION: Involved in the efflux of excess of L-lysine. This is
CC      necessary to control the intracellular L-lysine level (By
CC      similarity).
CC      -1- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass
CC      membrane protein (By similarity).
CC      -1- SIMILARITY: Belongs to the lysE/argo transporter (TC 2.A.75)
CC      family.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs License
CC      -----
DR      EMBL: AB083133; BAB88827.1; ALT_INIT; Genomic DNA.
DR      EMBL: BA000035; BAC18167.1; ALT_INIT; Genomic DNA.
DR      GenomesReviews; BA000035.GR; CE1357.
DR      BioCyc: CEFF196164:CE1357-MONOMER; -.
DR      InterPro: IPR001123; LysE.
DR      Pfam: PF01810; LysE; 1.
KM      Complete proteome; Inner membrane; Membrane; Transmembrane; Transport.
FT      CHAIN 1
FT      TRANSMEM 3 23
FT      TRANSMEM 37 57
FT      TRANSMEM 66 86
FT      TRANSMEM 139 159
FT      TRANSMEM 172 192
FT      TRANSMEM 208 228
SQ      SEQUENCE 228 AA; 24374 MW; 68FB379A8380EDA7 CRC64;

Query Match 62.8%; Score 389.5; DB 1; Length 228;
Best Local Similarity 65.8%; Pred. No. 6.8e-29;
Matches 79; Conservative 15; Mismatches 21; Indels 5; Gaps 2;

QY      4 MEIFITGLLGLASLLSIPQNVLVKQIGREGIAVLVCLISDVEFLTGLGVLL 63
DB      1 MEIFVTGLLGLASLLSIPQNVLVKQIGREGITAVIIVCLISDVLFTGLTGVLI 60

QY      64 SNAPIYVDIMRWGIAVLVFAVMAAKDAMTNKVEAPQIIETEPVDDTPIGVF 123
DB      61 SDTAPIIIDIRWCGIAVLVFAVMAAKDAMTNKVEAPQIIETEPVDDTPIGVF 115

RESULT 5
LysE_CORDI STANDARD; PRT; 228 AA.
ID LysE_CORDI STANDARD; PRT; 228 AA.
AC Q6NHPI;
DT 11-OCT-2004, integrated into UniProtKB/Swiss-Prot.
DT 05-JUN-2004, sequence version 1.
DT 07-MAR-2006, entry version 10.
DE Lysine exporter protein.
GN Name=lysE; Ordered locus names=DIP1091;
OS Corynebacterium diptheriae;
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OC NCBI_TaxID=1717;
RN [1]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC STRAIN=Biotype gravis / NCTC 13129;
RX MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;
RA Cedeno-Tarrega A.-M., Eferatiou A., Dover L.G., Holden M.T.G.,
RA Pallen M.J., Bentley S.D., Beara G.S., Churcher C.M., James K.D.,
RA De Zorja A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,
RA Hamlin N., Holtroyd S., Jagers K., Moule S., Quail M.A.,

```

```

RA      Rabinowitz E., Rutherford K.M., Thomson N.R., Unwin L.,
RA      Whitehead S., Bartell B.G., Parkhill J.;
RT      "The complete genome sequence and analysis of Corynebacterium
RT      diptheriae NCTC13129."
RL      Nucleic Acids Res. 31:6516-6523(2003).
CC      -1- FUNCTION: Involved in the efflux of excess of L-lysine. This is
CC      necessary to control the intracellular L-lysine level (By
CC      similarity).
CC      -1- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass
CC      membrane protein (By similarity).
CC      -1- SIMILARITY: Belongs to the lysE/argo transporter (TC 2.A.75)
CC      family.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs License
CC      -----
DR      EMBL: BX248357; CAE49614.1; -; Genomic DNA.
DR      GenomesReviews; BX248353.GR; DIP1091.
DR      BioCyc: CDIP1717:DIP1091-MONOMER; -.
DR      InterPro: IPR001123; LysE.
DR      Pfam: PF01810; LysE; 1.
KM      Complete proteome; Inner membrane; Membrane; Transmembrane; Transport.
FT      CHAIN 1
FT      TRANSMEM 4 26
FT      TRANSMEM 38 60
FT      TRANSMEM 65 87
FT      TRANSMEM 139 161
FT      TRANSMEM 171 193
FT      TRANSMEM 205 227
SQ      SEQUENCE 228 AA; 24662 MW; 6C5AD0D7CB3ADE7 CRC64;

Query Match 43.7%; Score 271; DB 1; Length 228;
Best Local Similarity 47.1%; Pred. No. 1.4e-17;
Matches 56; Conservative 22; Mismatches 37; Indels 4; Gaps 2;

QY      4 MEIFITGLLGLASLLSIPQNVLVKQIGREGIAVLVCLISDVEFLTGLGVLL 63
DB      1 MSINAGTLMGLSLVLAIGPNALIRQIGREGIPLVCLISDVLITGGINVGL 60

QY      64 SNAPIYVDIMRWGIAVLVFAVMAAKDAMTNKVEAPQIIETEPVDDTPIGV 119
DB      61 VDRAPIALVLMKGVAVLLYFPTCKEAPKRGQA-LAVEGSEPVAYEVDADSSGV 118

RESULT 6
ARGO_EC0L6 STANDARD; PRT; 211 AA.
ID ARGO_EC0L6 STANDARD; PRT; 211 AA.
AC Q8FE55;
DT 11-OCT-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2003, sequence version 1.
DT 07-MAR-2006, entry version 17.
DE Arginine exporter protein argo.
GN Name=argo; Ordered locus names=c3501;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=217992;
RN [1]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC STRAIN=OE:HI / CFT073 / ATCC 700928 / UPEC;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Rosach P.,
RA Raeko D., Buckles B.L., Lion S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT      of uropathogenic Escherichia coli."
CC -1- FUNCTION: Involved in the export of arginine. Important to control
CC      the intracellular level of arginine and the correct balance
CC      between arginine and lysine (By similarity).
CC      -1- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass

```

```

CC      membrane protein (By similarity).
CC      -|- INDUCTION: Transcriptionally regulated by argP. Lysine has a
CC      negative effect on the expression of argO (By similarity).
CC      -|- SIMILARITY: Belongs to the LysE/Argo transporter (TC 2.A.75)
CC      family.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL: AE016766; AAN81949.1; -; Genomic DNA.
DR      BioCyc: ECOLI99310:C3501-MONOMER; -
DR      HAMAP: MF_01901; -; 1.
DR      InterPro: IPR004777; Lys exporter.
DR      InterPro: IPR001123; LysE.
DR      Pfam: PF01810; LysE; 1.
DR      TIGRfam: TIGR00948; 2a75; 1.
KM      Amino-acid transporter; Complete proteome; Inner membrane; Membrane;
KM      Transmembrane; Transport.
FT      CHAIN          1          211
FT      TRANSMEM      1          21
FT      TOPO_DOM      22          36      Cytoplasmic (Potential).
FT      TRANSMEM      37          57      Potential.
FT      TOPO_DOM      58          67      Periplasmic (Potential).
FT      TRANSMEM      68          88      Potential.
FT      TOPO_DOM      89          110      Cytoplasmic (Potential).
FT      TRANSMEM      111         131      Potential.
FT      TOPO_DOM      132         146      Periplasmic (Potential).
FT      TRANSMEM      147         167      Potential.
FT      TOPO_DOM      168         181      Cytoplasmic (Potential).
FT      TRANSMEM      182         202      Potential.
FT      TOPO_DOM      203         211      Periplasmic (Potential).
SQ      SEQUENCE      211 AA; 23174 MW; 5F22D06A3A8FBD73 CRC64;

Query Match          34.5%; Score 214; DB 1; Length 211;
Best Local Similarity 35.8%; Pred. No. 3.7e-12;
Matches 48; Conservative 27; Mismatches 41; Indels 18; Gaps 3;

QY      7 FTGGLLGASLLISGPQNVLVKQIGKREGGLAVLVLCISDVFLFIAGTLGVDLISNA 66
DB      5 YFGGLALGAMMILPLGPQNAFVNMQGIKROYHIMILCALISDLVLCAGIFGGSALLMQ 64
QY      67 APIVLDIMRWGCIAYLWFAVMAKDMTKVE--APQIIIE-----TEPT 110
DB      65 SPWLLALVWVGVAFLWVGFGAFKTMSSNIELASAEVLKQGRWKIATMLAVTWLNP 124
QY      111 VPDDT--PLGVFGG 122
DB      125 VYLDTFVVLGSLGG 138

RESULT 7
ID      Q32BY3 SHIDS PRELIMINARY; PRT; 211 AA.
AC      Q32BY3.
DT      06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT      07-FEB-2006, sequence version 1.
DE      Hypothetical protein Y9GA.
GN      Name=Y9GA; OrderedLocNames=SDY_3159;
OS      Shigella dysenteriae serotype 1 (strain Sd197).
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Shigella.
OX      NCBI_TaxID=300267;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX      PubMed=16275786; DOI=10.1093/nar/gk1954;
RA      Wang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
RA      Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
RA      Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
RA      Qiang B., Hou Y., Yu J., Jin Q.
RT      "Genome dynamics and diversity of Shigella species, the etiologic
RT

```

```

RT      agents of bacillary dysentery."
RL      Nucleic Acids Res. 33:6445-6458(2005).
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL: CP000034; ABB63172.1; -; Genomic DNA.
DR      GO: GO:0016021; C: integral to membrane; IEA.
DR      GO: GO:0016020; C: membrane; IEA.
DR      GO: GO:0005293; F: lysine permease activity; IEA.
DR      GO: GO:0006865; P: amino acid transport; IEA.
KM      Complete proteome; Hypothetical protein.
SQ      SEQUENCE      211 AA; 23174 MW; 5F22D06A3A8FBD73 CRC64;

Query Match          34.5%; Score 214; DB 2; Length 211;
Best Local Similarity 35.8%; Pred. No. 3.7e-12;
Matches 48; Conservative 27; Mismatches 41; Indels 18; Gaps 3;

QY      7 FTGGLLGASLLISGPQNVLVKQIGKREGGLAVLVLCISDVFLFIAGTLGVDLISNA 66
DB      5 YFGGLALGAMMILPLGPQNAFVNMQGIKROYHIMILCALISDLVLCAGIFGGSALLMQ 64
QY      67 APIVLDIMRWGCIAYLWFAVMAKDMTKVE--APQIIIE-----TEPT 110
DB      65 SPWLLALVWVGVAFLWVGFGAFKTMSSNIELASAEVLKQGRWKIATMLAVTWLNP 124
QY      111 VPDDT--PLGVFGG 122
DB      125 VYLDTFVVLGSLGG 138

RESULT 8
ID      ARGO_ECOLI STANDARD; PRT; 211 AA.
AC      P11667.
DT      01-OCT-1989, integrated into UniProtKB/Swiss-Prot.
DT      01-OCT-1996, sequence version 2.
DT      07-MAR-2006, entry version 55.
DE      Arginine exporter protein argO.
GN      Name=argo; OrderedLocNames=b2923;
OS      Escherichia coli.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Escherichia.
OX      NCBI_TaxID=562;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=K12 / MG1655;
RX      MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA      Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA      Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA      Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA      Mau B., Shao Y.
RT      "The complete genome sequence of Escherichia coli K-12."
RT      Science 277:1453-1474(1997).
RL      [2]
RP      NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 15-211.
RC      STRAIN=K12 / GS520;
RX      MEDLINE=89313302; PubMed=2546007;
RA      Alefunder P.R., Pernam R.N.
RT      "Identification, molecular cloning and sequence analysis of a gene
RT      cluster encoding the class II fructose 1,6-bisphosphate aldolase, 3-
RT      phosphate dehydrogenase and a putative second glyceraldehyde 3-
RT      mol. Microbiol. 3:723-732(1989).
RL      [3]
RN      [3]
RP      FUNCTION.
RC      STRAIN=K12;
RX      PubMed=15150242; DOI=10.1126/JB.186.11.3539-3546.2004;
RA      Nandineni M.R., Gowrishankar J.
RT      "Evidence for an arginine exporter encoded by y9GA (argo) that is
RT      regulated by the LysR-type transcriptional regulator Argp in
RT      Escherichia coli."
RL      J. Bacteriol. 186:3539-3546(2004).

```


RN [4]
 RP TOPOLOGY.
 RC STRAIN=K12 / MG1655;
 RX PubMed=15919996; DOI=10.1126/science.1109730;
 RT "Global topology analysis of the Escherichia coli inner membrane
 RT proteome."
 CC Science 308:1321-1323(2005).
 CC -1- FUNCTION: Involved in the export of arginine. Important to control
 CC the intracellular level of arginine and the correct balance
 CC between arginine and lysine. May also be involved in the export of
 CC canavanine (a plant-derived antimetabolite).
 CC -1- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass
 CC membrane protein.
 CC -1- INDUCTION: Transcriptionally regulated by argP in response to the
 CC accumulation of intracellular arginine or canavanine. Lysine has a
 CC negative effect on the expression of argO.
 CC -1- SIMILARITY: Belongs to the lysE/argO transporter (TC 2.A.75)
 CC family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC
 CC EMBL: U28377; AAA69090.1; -; Genomic DNA.
 CC EMBL: U00096; AAC75960.1; -; Genomic DNA.
 CC EMBL: X14436; CAA32607.1; -; Genomic DNA.
 CC PIR: B65077; OOECSA.
 CC GenomeReviews: U00096_GR; b2923.
 CC Echobase: EB1148; -;
 CC Ecogene: EG1159; argO.
 CC Biocyc: Ecocyc:YGA-MONOMER; -;
 CC LinkHub: P11667; -;
 CC HAMAP: MF_01901; -; 1.
 CC InterPro: IPR004777; Lys exporter.
 CC InterPro: IPR001123; LysE.
 CC Pfam: PF01810; LysE; 1.
 CC TIGRFAMs: TIGR00948; 2a75; 1.
 CC Amino-acid transport; Complete proteome; Inner membrane; Membrane;
 CC Transmembrane; Transport.
 FT CHAIN 1 211
 FT TRANSMEM 1 21
 FT TOPO_DOM 22 36
 FT TRANSMEM 37 57
 FT TOPO_DOM 58 67
 FT TRANSMEM 68 88
 FT TOPO_DOM 89 110
 FT TRANSMEM 111 131
 FT TOPO_DOM 132 146
 FT TRANSMEM 147 167
 FT TOPO_DOM 168 178
 FT TRANSMEM 179 199
 FT TOPO_DOM 200 211
 FT SEQUENCE 211 AA; 23176 MW; 2DAFE27B6A9BBE22 CRC64;
 SQ
 Query Match 34.4%; Score 213; DB 1; Length 211;
 Best Local Similarity 43.0%; Pred. No. 4.6e-12;
 Matches 40; Conservative 21; Mismatches 32; Indels 0; Gaps 0;

DT 21-FEB-2006, sequence version 1.
 DT 07-MAR-2006, entry version 2.
 DE Arginine transporter.
 GN Name=argO;
 OS Escherichia coli W3110.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OC NCBI_TaxID=316407;
 RP (1)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RA MEDLINE=81053692; PubMed=6159575;
 RA Smith D.R., Calvo J.M.;
 RT "Nucleotide sequence of the E coli gene coding for dihydrofolate
 RT reductase."
 RL Nucleic Acids Res. 8:2255-2274(1980).
 RN (2)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RA Sekiguchi T., Ortega-Cesena J., Nosoh Y., Ohashi S., Tsuda K.,
 RT "DNA and amino-acid sequences of 3-isopropylmalate dehydrogenase of
 RT Bacillus coagulans. Comparison with the enzymes of Saccharomyces
 RT cerevisiae and Thermus thermophilus."
 RL Biochim. Biophys. Acta 867:36-44(1986).
 RN (3)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RA Chen H., Sun Y., Stark T., Beattie W., Moses R.E.;
 RT "Nucleotide sequence and deletion analysis of the polB gene of
 RT Escherichia coli."
 RL DNA Cell Biol. 9:613-635(1990).
 RN (4)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RA Smallshaw J.E., Kelln R.A.;
 RT "Cloning, nucleotide sequence and expression of the Escherichia coli
 RT K-12 pyrH gene encoding UMP kinase."
 RL Genetics (LIFE Sci. Adv.) 11:59-65(1992).
 RN (5)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RA Hayashi K., Murooka N., Yamamoto Y., Fujita K., Isono K., Choi S.,
 RA Ohtsubo E., Baba T., Wanner B.L., Mori H., Horiuchi T.;
 RT "Highly accurate genome sequences of Escherichia coli K-12 strains
 RT MG1655 and W3110."
 RL Mol. Syst. Biol. 0:0-0(2006).
 RN (6)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RA PubMed=16397293; DOI=10.1093/nar/gk150;
 RA Riley M., Abe T., Arnaud M.B., Berlyn M.K., Blattner F.R.,
 RA Chaudhuri R.R., Glaesner J.D., Horiuchi T., Kessler I.M., Kogaue T.,
 RA Mori H., Perna N.T., Plunkett G. III, Rudd K.E., Serres M.H.,
 RA Thomas G.H., Thomson N.R., Wishart D., Wanner B.L.;
 RT "Escherichia coli K-12: a cooperatively developed annotation snapshot-
 RT 2005."
 RL Nucleic Acids Res. 34:1-9(2006).
 RN (7)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RA MEDLINE=97349980; PubMed=9205837; DOI=10.1093/dnares/4.2.91;
 RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
 RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
 RA Oshima T., Oyama S., Saito N., Sampaio G., Satoh Y., Sivasubraman S.,
 RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
 RA Yamagata S., Horiuchi T.;
 RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
 RT K-12 genome corresponding to 50.0-68.8 min on the linkage map and
 RT DNA Res. 4:91-113(1997).
 RN (8)

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=97251355; PubMed=9097040; DOI=10.1093/dnares/3.6.379;
 RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
 RA Kasai H., Kimura S., Kikawa M., Kitagawa M., Makino K., Miki T.,
 RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
 RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,
 RA Sivasubramanian S., Tagami H., Takada J., Takemoto K., Wada C.,
 RA Yamamoto Y., Horiiuchi T.,
 RT "A 460-kb DNA sequence of the *Escherichia coli* K-12 genome
 RT corresponding to the 40.1-50.0 min region on the linkage map."
 RL DNA Res. 3:379-392(1996).
 [9]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=97251357; PubMed=9097039; DOI=10.1093/dnares/3.6.363;
 RA Itoh T., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
 RA Kasai H., Kashtamoto K., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
 RA Sempel G., Seki Y., Sivasubramanian S., Tagami H., Takada J.,
 RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiiuchi T.,
 RT "A 570-kb DNA sequence of the *Escherichia coli* K-12 genome
 RT corresponding to the 28.0-40.1 min region on the linkage map."
 RL DNA Res. 3:363-377(1996).
 [10]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=97094878; PubMed=8940112; DOI=10.1074/jbc.271.49.31145;
 RA Arn E.A., Abelson J.N.,
 RT "The 2'-5' RNA ligase of *Escherichia coli*. Purification, cloning, and
 RT genomic disruption."
 RL J. Biol. Chem. 271:31145-31153(1996).
 [11]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=97061202; PubMed=8905232; DOI=10.1093/dnares/3.3.137;
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashtamoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiiuchi T.,
 RT "A 718-kb DNA sequence of the *Escherichia coli* K-12 genome
 RT corresponding to the 12.7-28.0 min region on the linkage map."
 RL DNA Res. 3:137-155(1996).
 [12]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=94261430; PubMed=8202364;
 RA Fujita N., Mori H., Yura T., Ishihama A.,
 RT "Systematic sequencing of the *Escherichia coli* genome: analysis of the
 RT Nucleic Acids Res. 22:1637-1639(1994).
 [13]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=94240115; PubMed=8183897;
 RA Janosi L., Shimizu T., Kaji A.,
 RT "Ribosome recycling factor (ribosome releasing factor) is essential
 RT for bacterial growth."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:4249-4253(1994).
 [14]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=94124004; PubMed=7904973; DOI=10.1016/0378-1119(93)90470-N;
 RA Allikmets R., Gerrard B.C., Court D., Dean M.C.,
 RT "Cloning and organization of the abc and mdl genes of *Escherichia*
 RT coli: relationship to eukaryotic multidrug resistance."
 RL Gene 136:231-236(1993).
 [15]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;

RX MEDLINE=94018640; PubMed=8412694;
 RA van Heeswijk W.C., Rabenberg M., Westerhoff H.V., Kahn D.D.,
 RT "The genes of the glutamine synthetase adenylylation cascade are not
 RT regulated by nitrogen in *Escherichia coli*."
 RL Mol. Microbiol. 9:443-458(1993).
 [16]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=93259920; PubMed=8387990;
 RA Zhao S., Sandt C.H., Feulner G., Viazny D.A., Gray J.A., Hill C.W.,
 RT "The elements of *Escherichia coli* K-12: complex composites of shared
 RT and unique components that have different evolutionary histories."
 RL J. Bacteriol. 175:2799-2808(1993).
 [17]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=93123180; PubMed=8419307;
 RA Yamada M., Asaka S., Saiter M.H., Jr., Yamada Y.,
 RT "Characterization of the *gcd* gene from *Escherichia coli* K-12 W3110 and
 RT regulation of its expression."
 RL J. Bacteriol. 175:568-571(1993).
 [18]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=93116053; PubMed=1474579;
 RA Cormack R.S., Mackie G.A.,
 RT "Structural requirements for the processing of *Escherichia coli* 5 S
 RT ribosomal RNA by RNase E in vitro."
 RL J. Mol. Biol. 228:1078-1090(1992).
 [19]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=93094132; PubMed=1459951;
 RA Gervais F.G., Drapeau G.R.,
 RT "Identification, cloning, and characterization of *rcsf*, a new
 RT regulator gene for exopolysaccharide synthesis that suppresses the
 RT division mutation *ftsZ84* in *Escherichia coli* K-12."
 RL J. Bacteriol. 174:8016-8022(1992).
 [20]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=93077430; PubMed=1447125;
 RA Yamanaka K., Ogura T., Niki H., Hiraga S.,
 RT "Identification and characterization of the *smbA* gene, a suppressor of
 RT the *mukB* null mutant of *Escherichia coli*."
 RL J. Bacteriol. 174:7517-7526(1992).
 [21]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=93011013; PubMed=1396599;
 RA Condon C., Phillips J., Fu Z.Y., Squires C., Squires C.L.,
 RT "Query Match 34.4%; Score 213; DB 2; Length 211;
 RT Best Local Similarity 43.0%; Pred. No. 4,6e-12;
 RT Matches 40; Conservative 21; Mismatches 32; Indels 0; Gaps 0;
 RT
 QY 7 FTGGLGSLLSLSTGPQNVLYIKGIRKREGIAVLVLTLDVFLNAGTIGVLLSNA 66
 Db 5 YFOGALGAMLPGLPQPAFVFNQGIROYHIMALLCAISDLVLCIGIRGGSALLMO 64
 QY 67 APIVDIMRGGIAVLVFAVMAARDATNKVE 99
 Db 65 SPWLALVTVGVAFLVWYGFQAFRTASSNIE 97
 RESULT 10
 Q3YXU9 SHISS PRELIMINARY; PRT; 211 AA.
 AC Q3YXU9;
 DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 27-SEP-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Hypothetical protein Y99A.

```

GN Name=y99A; OrderedLocNames=SSO_3075; ORFNames=SSO_3075;
OS Shigella sonnei (strain Sso46).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
NCBI_TaxID=300269;
RN
  1)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16275786; DOI=10.1093/nar/gki1954;
RA Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
RA Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
RA Nie H., Peng Y., Xu J., Wang Y., Yan Z., Wen Y., Yao Z., Shen Y.,
RA Qiang B., Hou Y., Yu J., Jin Q.;
RT "Genome dynamics and diversity of Shigella species, the etiologic
RT agents of bacillary dysentery."
RL Nucleic Acids Res. 33:6445-6458(2005).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL, CP000038; AA289663.1; -; Genomic DNA.
DR GO, GO:0016021; C:integral to membrane; IEA.
DR GO, GO:0016020; C:membrane; IEA.
DR GO, GO:0005293; F:Lysine permease activity; IEA.
DR GO, GO:0006865; P:amino acid transport; IEA.
DR InterPro, IPR003016; Lipoyl BS.
DR InterPro, IPR004777; Lys exporter.
DR InterPro, IPR001123; LysE.
DR Pfam, PF01810; LysE; 1.
DR TIGRFAMs, TIGR00948; 2a75; 1.
DR PROSITE, PS00189; LIPOYL, UNKNOWN.1.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 211 AA; 23174 MW; DC946439D9EB920 CRC64;

```

```

RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN
  12)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / Sakai / RMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796; DOI=10.1093/dnares/8.1.11;
RA Hayashi T., Makino K., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Saekawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shingawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
CC
CC -1- FUNCTION: Involved in the export of arginine. Important to control
CC the intracellular level of arginine and the correct balance
CC between arginine and lysine (by similarity).
CC -1- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass
CC membrane protein (By similarity).
CC -1- INDUCTION: Transcriptionally regulated by argP. Lysine has a
CC negative effect on the expression of argO (By similarity).
CC -1- SIMILARITY: Belongs to the lysE/argO transporter (TC 2.A.75)
CC family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL, AE005174; AAG58049.1; -; Genomic DNA.
DR EMBL, BA000007; BAB37217.1; -; Genomic DNA.
DR PIR, B91103; B91103.
DR PIR, E85948; E85948.
DR GenomeReviews, BA000007 GR; EC83794.
DR GenomeReviews, AE005174 GR; 24260.
DR BioCyc, ECOL83334-1; EC83794-MONOMER; -.
DR HAMAP, MF_01901; -, 1.
DR InterPro, IPR004777; Lys_exporter.
DR InterPro, IPR001123; LysE.
DR Pfam, PF01810; LysE; 1.
DR TIGRFAMs, TIGR00948; 2a75; 1.
DR AMIGO, ECOL83334-1; EC83794-MONOMER; -.
KW Amino-acid transport; Complete proteome; Inner membrane; Membrane;
KW Transmembrane; Transport.
FT CHAIN 1..211
FT FT
FT TRANSMEM 1..211 /FTid=PRO_0000204159.
FT FT
FT TOPO_DOM 22..36 Potential.
FT TRANSMEM 37..57 Cytoplasmic (Potential).
FT TOPO_DOM 58..67 Potential.
FT TRANSMEM 68..67 Periplasmic (Potential).
FT TOPO_DOM 89..110 Potential.
FT TRANSMEM 111..131 Cytoplasmic (Potential).
FT TOPO_DOM 132..146 Potential.
FT TRANSMEM 147..167 Periplasmic (Potential).
FT TOPO_DOM 168..181 Potential.
FT TRANSMEM 182..202 Cytoplasmic (Potential).
FT TOPO_DOM 203..211 Periplasmic (Potential).
SQ SEQUENCE 211 AA; 23202 MW; 4422D078B182266C CRC64;

```

```

Query Match 33.9%; Score 210; DB 2; Length 211;
Best Local Similarity 35.1%; Pred. No. 5.7e-12;
Matches 47; Conservative 28; Mismatches 41; Indels 18; Gaps 3;

```

```

Query Match 33.9%; Score 210; DB 1; Length 211;
Best Local Similarity 35.1%; Pred. No. 8.8e-12;
Matches 47; Conservative 27; Mismatches 42; Indels 18; Gaps 3;

```

[illegible]

Query Match	Score	DB	Length
Best Local Similarity	35.1%	Pred. No. 8,8e-12;	
Matches 47; Conservative 27; Mismatches 42; Indels 18; Gaps 3			
QY 7 FITGALLGASLLISGPNVAVIKQIGKREGIAVLAVCLISDPVLFIAGTGAVDLSNA 66			
Db 5 YFGALGAGAMILPLGPNQNAFVWNOGIRRYHIMIALCALISDVLICAGIFGGSALLMQ 64			
QY 67 APIVLDIMRWGIAVYLWFAVMAAKDAMTNKVE--APQIIIEE-----TEPT 110			
Db 65 SPMLLATVWGGVFFLLWYGFAGFKTAMSSNIELASAEVLKQGRWKIIATMLAVTMLNPH 124			
QY 111 VPDDT--PLGVFGG 122			
Db 125 VYLDTFVVLGSLGG 138			

RESULT 13

Q31W12.SHIBS

ID Q31W12.SHIBS PRELIMINARY; PRT; 211 AA.

AC 06-DEC-2005, integrated into UniProtKB/TrEMBL.

DT 06-DEC-2005, sequence version 1.

DT 07-FEB-2006, entry version 4.

DE Hypothetical protein ysgA.

GN Name=ysgA; Ordered locus names=SBO_3070;

OS Shigella boydii serotype 4 (strain SD227).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Shigella.

OX NCBI_Taxid=300268;

[1]

NP_011111.1 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RefSeq: NC_011111.1 PubMed:16275786; DOI=10.1093/nar/gk1954.

Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X., Ra Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S., Qian H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y., Qiang B., Hou Y., Yu J., Jin Q.;

"Genome dynamics and diversity of Shigella species, the etiologic agents of bacillary dysentery";

Nucleic Acids Res. 33:6445-6458(2005).

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NonCommercial License

CC

DR EMBL: CP000036; ABB67576.1; -; Genomic DNA.

DR GO: GO:0016021; C: integral to membrane; IEA.

DR GO: GO:0016020; C: membrane; IEA.

DR GO: GO:0005293; F: lysine permease activity; IEA.

DR GO: GO:0006865; P: amino acid transport; IEA.

KW Complete proteome; Hypothetical protein.

SEQUENCE 211 AA; 23246 MW; 42968395506758D CRC64;

Query Match

Best Local Similarity 33.4%; Score 207; DB 2; Length 211;

Matches 47; Conservative 27; Mismatches 42; Indels 18; Gaps 3;

RESULT 14

RRGO_SALT1

ID	ARGO_SALT1	STANDARD;	PRT;	211 AA.
AD	08Z3I2;	07CTC3;		
DT	11-OCT-2004,	integrated into UniProtKB/Swiss-Prot.		
DT	01-MAR-2002,	sequence version 1.		
DE	Arginine exporter protein argO.			
GN	Name=argO; Ordered locus names=STY3222, t2984;			
OS	Salmonella typhi.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Salmonella.			
NCBI	_taxid=601;			
RM	11			
RP	NCBI			
RC	STRAIN=CT18;			
RX	MEDLINE=21534947; PubMed=11677608; DOI=10.1098/35101607;			
RA	Parthini C.J., Dougan G., James K.D., Thomson N.R., Pickett D., Wain J.,			
RA	Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,			
RA	Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,			
RA	Crofton A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,			
RA	Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,			
RA	Krogsh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,			
RA	Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,			
RA	Whitehead S., Barrett B.G.;			
RT	"Complete genome sequence of a multiple drug resistant Salmonella			
RT	enterica serovar Typhi CT18."			
RL	Nature 413:848-852 (2001).			
RM	12			
RP	NCBI			
RC	STRAIN=Ty2; ATCC 700931.			
RX	MEDLINE=22531367; PubMed=12644504;			
RX	DOI=10.1128/JB.185.7.2330-2337.2003;			
RA	Deng W., Ilov S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,			
RA	Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;			
RT	"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2			
RT	and CT18."			
RL	J. Bacteriol. 185:2330-2337 (2003).			
CC	-I- FUNCTION: Involved in the export of arginine. Important to control			
CC	the intracellular level of arginine and the correct balance			
CC	between arginine and lysine (By similarity).			
CC	-I- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass			
CC	membrane protein (By similarity).			
CC	-I- SIMILARITY: Belongs to the lysE/argO transporter (TIC 2.A.75)			
CC	family.			
CC	-----			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NonCommercial license			
CC	-----			
DR	EMBL; AL627277; CA02896.1; -; Genomic DNA.			
DR	EMBL; AE014613; AAO70536.1; -; Genomic DNA.			
DR	GenomeReviews; AL513382.GR; STY3222.			
DR	GenomeReviews; AE014613.GR; t2984.			
DR	BioCyc; SENT209261:t2984-MONOMER; -			
DR	BioCyc; SENT90370:STY3222-MONOMER; -			
DR	HAMAP; MF_01901; -; 1.			
DR	InterPro; IPR004777; LysE exporter.			
DR	InterPro; IPR001123; LysE.			
DR	Pfam; PF01810; LysE; 1.			
DR	TIGRFAMs; TIGR00948; 2a75; 1.			
KW	Amino-acid transporter; Complete proteome; Inner membrane; Membrane;			
KW	Transmembrane; Transport.			
FT	CHAIN	1	211	
FT	TRANSMEM	1	21	
FT	TOPO_DOM	22	36	
FT	TRANSMEM	37	57	
FT	TOPO_DOM	58	67	
FT	TRANSMEM	68	88	
FT	TOPO_DOM	89	110	
FT	TRANSMEM	111	131	
FT	TOPO_DOM	132	146	
FT	TRANSMEM	147	167	
FT	TOPO_DOM	168	178	
FT	TRANSMEM	179	199	

```

FT      TOPO DOM      200      211      Periplasmic (Potential).
SQ      SEQUENCE      211 AA; 23172 MW; 13CB427CAB5A3FC CRC64;
Query Match
Best Local Similarity 38.1%; Score 205; DB 1; Length 211;
Matches 37; Conservative 26; Mismatches 34; Indels 0; Gaps 0
QY      3 IMEIFITGLLLGASLLISIGPQNVLYIKQIKREGILAVLLVCLISDVFIAGTIGVDL 62
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1 MSYFQGVALLGAMILLPGPONAFVFMQGIIRQYHMLIALCALSDLVLSIGIFGSA 60
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      63 LSMAPIVLDIMKNGIAYLLMFVAWAADANTNKYE 99
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      61 LLMQSPWLLALVTWGVAFLLWYFGCALXTAMSNMLE 97
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
ARGO_SALCH
ID      ARGO_SALCH      STANDARD;      PRT;      211 AA.
AC      Q57K48;
DT      25-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT      10-MAY-2005, sequence version 1.
DT      07-MAR-2006, entry version 8.
DE      Arginine exporter protein argo.
GN      Name=argo; OrderedLocustNames=SC3008;
OS      Salmonella choleraesuis.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Salmonella.
OX      NCBI_Taxid=591;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=SC-B67;
RA      PubMed=15781495; DOI=10.1093/nar/gk1297;
RA      Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
RA      Wang H.-S., Lee Y.-S.;
RT      "The genome sequence of Salmonella enterica serovar Choleraesuis, a
RL      highly invasive and resistant zoonotic pathogen.";
RL      Nucleic Acids Res. 33:1690-1698(2005).
CC      -1- FUNCTION: Involved in the export of arginine. Important to control
CC      the intracellular level of arginine and the correct balance
CC      between arginine and lysine (By similarity).
CC      -1- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass
CC      membrane protein (By similarity).
CC      -1- SIMILARITY: Belongs to the lysE/argo transporter (TC 2.A.75)
CC      family.
-----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs License
CC      EMBL; AE017220; AAX66914.1; -1- Genomic_DNA.
CC      GenomeReviews; AE017220_GR; SC3008.
DR      HAMAP; MF_01901; -1-
DR      InterPro; IPR004777; Lys_exporter.
DR      InterPro; IPR01123; LysE.
DR      Pfam; PF01810; LysE; 1.
DR      TIGRFAMs; TIGR00948; 2a75; 1.
KW      Amino-acid transport; Complete proteome; Inner membrane; Membrane;
KW      Transmembrane; Transport.
FT      CHAIN      1      211
FT      TRANSMEM      1      21
FT      TRANSMEM      37      57      Potential.
FT      TRANSMEM      68      88      Potential.
FT      TRANSMEM      111      131      Potential.
FT      TRANSMEM      147      167      Potential.
FT      TRANSMEM      179      199      Potential.
SQ      SEQUENCE      211 AA; 23239 MW; 64D626F0B3F1D0F CRC64;

Query March      32.9%; Score 204; DB 1; Length 211;
Best Local Similarity 38.1%; Pred. No. 3,3e-11;
Matches 37; Conservative 25; Mismatches 35; Indels 0; Gaps 0;
3 IMEIFITGLLLGASLLISIGPQNVLYIKQIKREGILAVLLVCLISDVFIAGTIGVDL 62

```

Db 1 MISTYFQGFALGAMMILPLGPNAPVMMQGIROTHMLIALLCALSDLVISAGIFGGA 60
QY 63 LSNAPIVLDIMRWGIAVLLMFVMAKADAMTKVE 99
Db 61 LMQSPWILALVTWGVAFILWGFGLKXTAMSSNLE 97

Search completed: July 19, 2006, 00:30:30
Job time : 302 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2006, 00:30:55 ; Search time 51 Seconds
(without alignments)
212.820 Million cell updates/sec

Title: US-10-716-470-10

Perfect score: 620
Sequence: 1 MVMEIFITGLLGASLLLS.....EEETPTVDDPTPLGVFGGCH 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA: *
1: /EMC_Celeerra_SIDS3/ptodata/2/1aa/5_COMB.pep: *
2: /EMC_Celeerra_SIDS3/ptodata/2/1aa/6_COMB.pep: *
3: /EMC_Celeerra_SIDS3/ptodata/2/1aa/7_COMB.pep: *
4: /EMC_Celeerra_SIDS3/ptodata/2/1aa/H_COMB.pep: *
5: /EMC_Celeerra_SIDS3/ptodata/2/1aa/PTUS_COMB.pep: *
6: /EMC_Celeerra_SIDS3/ptodata/2/1aa/RE_COMB.pep: *
7: /EMC_Celeerra_SIDS3/ptodata/2/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	584	94.2	236	2	US-09-105-117K-2
2	215	34.7	211	2	US-09-459-573-16
3	205	33.1	213	2	US-09-489-039A-11845
4	185	29.8	214	2	US-09-543-681A-4972
5	172.5	27.8	232	2	US-09-252-991A-24479
6	158	25.5	211	2	US-09-328-352-5737
7	112	18.1	211	2	US-09-902-540-9913
8	109	17.6	219	2	US-09-489-039A-7731
9	99.5	16.0	212	2	US-09-543-681A-7767
10	93.5	15.1	235	2	US-09-328-352-8249
11	90.5	14.6	208	2	US-09-328-352-5111
12	88.5	14.3	212	2	US-09-459-573-12
13	88	14.2	211	2	US-09-489-039A-9608
14	86.5	14.0	205	2	US-09-489-039A-12661
15	86	13.9	206	2	US-09-252-991A-18746
16	86	13.9	260	2	US-09-252-991A-25992
17	83.5	13.5	210	2	US-09-328-352-4775
18	83.5	13.5	222	2	US-09-252-991A-26644
19	83	13.4	552	2	US-09-489-039A-7419
20	80.5	13.0	228	2	US-09-543-681A-4854
21	79.5	12.8	205	2	US-09-396-357-2
22	79.5	12.8	205	2	US-09-847-392-2
23	79.5	12.8	221	2	US-09-328-352-6659
24	79.5	12.8	250	2	US-09-543-681A-4487
25	79	12.7	212	2	US-09-248-796A-20354
26	77.5	12.5	195	2	US-09-459-573-14

27	77.5	12.5	249	2	US-09-252-991A-25717	Sequence 25717, A
28	76.5	12.3	317	2	US-09-489-039A-8076	Sequence 8076, Ap
29	75	12.1	216	2	US-09-540-236-3467	Sequence 3467, Ap
30	74.5	12.0	1172	2	US-09-328-352-6071	Sequence 6071, Ap
31	74	11.9	213	2	US-09-252-991A-16947	Sequence 16947, A
32	74	11.9	302	2	US-09-252-991A-22091	Sequence 22091, A
33	73.5	11.9	214	2	US-09-489-039A-9793	Sequence 9793, Ap
34	73.5	11.9	238	2	US-09-328-352-7122	Sequence 7122, Ap
35	73.5	11.9	464	2	US-09-489-039A-9621	Sequence 9621, Ap
36	73	11.8	222	2	US-09-328-352-6471	Sequence 6471, Ap
37	73	11.8	237	2	US-09-252-991A-27175	Sequence 27175, A
38	72.5	11.7	256	2	US-09-270-767-47525	Sequence 47525, A
39	72	11.6	211	2	US-09-252-991A-20747	Sequence 20747, A
40	72	11.6	427	2	US-09-721-870-117	Sequence 117, App
41	72	11.6	434	2	US-09-721-870-117	Sequence 117, App
42	72	11.6	446	2	US-09-602-787A-426	Sequence 426, App
43	71.5	11.5	223	2	US-09-459-573-10	Sequence 10, Appl
44	71.5	11.5	461	2	US-09-248-796A-23597	Sequence 23597, A
45	70.5	11.4	257	2	US-09-560-761B-12	Sequence 12, Appl

ALIGNMENTS

```

RESULT 1
; US-09-105-117K-2
; Sequence 2, Application US/09105117K
; Patent No. 6858406
; GENERAL INFORMATION:
; APPLICANT: Forschungszentrum Juelich GmbH; Marina Vrljic et al.
; TITLE OF INVENTION: Process for the microbial production of amino acids by
; FILE OF INVENTION: Boosted activity of export carriers
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/09/105.117K
; CURRENT FILING DATE: 1996-06-17
; PRIOR APPLICATION NUMBER: PCT/DE96/02485
; PRIOR FILING DATE: 1996-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: (lyse)
US-09-105-117K-2

Query Match          94.2%; Score 584; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MVMEIFITGLLGASLLISGPNVLYKQIRREGIAVLVCLISDVFLEAGTGV 60
DB      1  MVMEIFITGLLGASLLISGPNVLYKQIRREGIAVLVCLISDVFLEAGTGV 60

QY      61  DLISNAPIVDINRWGIAVLWFVAWAADANTNKVAPQIEETPTVDDPTPLG 118
DB      61  DLISNAPIVDINRWGIAVLWFVAWAADANTNKVAPQIEETPTVDDPTPLG 118

RESULT 2
US-09-459-573-16
; Sequence 16, Application US/09459573
; Patent No. 6979560
; GENERAL INFORMATION:
; APPLICANT: LIVSHITS, VITALITY
; APPLICANT: ZAKATAEVA, NATALIA
; APPLICANT: NAKANISHI, KAZUO
; APPLICANT: VENIAMINOVICH, VLADIMIR
; APPLICANT: TROSHIN, PETR
; APPLICANT: TOKMAKOVA, IRINA
; TITLE OF INVENTION: METHOD FOR PRODUCING L-AMINO ACIDS
; FILE REFERENCE: 0010-1066-0

```

```

? CURRENT APPLICATION NUMBER: US/09/459,573
? CURRENT FILING DATE: 1999-12-13
? PRIOR APPLICATION NUMBER: RU96124016
? PRIOR FILING DATE: 1996-12-30
? PRIOR APPLICATION NUMBER: RU99104431
? PRIOR FILING DATE: 1999-03-09
? NUMBER OF SEQ ID NOS: 24
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 16
? LENGTH: 211
? TYPE: PRY
? ORGANISM: Escherichia coli
US-09-459-573-16

```

Query Match	34.7%	Score 215;	DB 2;	Length 211;
Best Local Similarity	41.2%;	Pred. No. 1.3e-19;		
Matches 40;	Conservative 22;	Mismatches 35;	Indels 0;	Gaps 0;

Db **Q**y
 3 IMEIFITGLLGASLLSISGPQNVLVIGKIKREGLIALLVLCISDVFLFIAGTIGVDL 62
 | | | | : : | | : : | | : : | | : :
1 VFSYFQGGLAQAAILPLGPNQAFVMNQIRQYHIMITALCAISDLVLCIAGIPGGSA 60

DQ 63 LSNAPVLDIMRWGIAVLWFAVMALADAMTNKYE 99
| : : : : : : | : : :
Db 61 LTMGPWLIALVTWGVAELTWYGFAGFTAMSSNIE 97

RESULT 3
US-09-48

```

US-09-489-039A-11845
; Sequence 11845, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709, 2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11845
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-11845

```

Query Match	33.1%	Score 205;	DB 2;	Length 213;
Best Local Similarity	37.4%	Pred. No. 2.7e-19;		
Matches 37; Conservative	25;	Mismatches 37;	Indels 0;	Gaps 0;

QY 1 MWIIEIFITGLLGASLLISIPQNVLYIKQIKREGGLAVLVCILSDVLPFIAGTLGV 600
::: |||::: |||: |||: : : : |||
Db 1 ILMTYYFQGLALGAAMILPLSPQNAFVNWQIGIRQYHMLIALLCVSDLLICAGIEGG 600

```

QY      61 DLISNAPIVLDIRMGGIAYLLNFAVMAAKDAMTKVE 99
          | : | : | | : | | : | | : | | : |
Db      61 SALIMQSPWLLATVTWGVAFLLMTWFGALKTAFSGSLE 99

```

RESULT 4
ITS-09-54

```

US-09-543-681A-4972
; Sequence 4972, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09

```

```

; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4972
; LENGTH: 214
; TYPE: prt
; ORGANISM: Proteus mirabilis
US-09-543-681A-4972

```

Query Match	29.8%;	Score 185;	DB 2;	Length 214;
Best Local Similarity	36.0%;	Pred. No. 1.1e-15;		
Matches 36;	Conservative 22;	Mismatches 42;	Indels 0;	Gaps 0;

QY 3 IMELFITGLLGASLLISGPQNVLIKQGIKREGLIYLVLCILSDVFLEIAGTIGVDL 62
 :: ||| ::||| ::||| :: : ||| |
 Db 8 MLTTFQGGFLISAMILPIGAQNAFVLQQGSKQYHLSAFLCALSDVILISGIVFGGSA 67

```

QY      63  LSNAPIVLDIRMGCIAYLLMFVMAAKADAMTNKVEAPQ 102
        |  ::  ::  |||  ::  |||  |  |  |  |  |  |
Db      68  LLSQSEYLLILLITWGVAFLLMYGWNAPKTAFTKEIELSQ 107

```

RESULT 5

```

: Sequence 24479, Application US/09252991A
: Patent No. 6551795
:
: GENERAL INFORMATION:
: APPLICANT: Marc J. Rubenfield et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
: FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196.136
: CURRENT APPLICATION NUMBER: US/09/252,991A
: CURRENT FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ ID NOS: 33142
: SEQ ID NO 24479
: LENGTH: 232
: TYPE: PRF
: ORGANISM: Pseudomonas aeruginosa
:
: IS-09-252-991A-24479

```

Query Match	27.8%;	Score 172.5;	DB 2;	Length 232;
Best Local Similarity	35.7%;	Pred. No. 5e-14;		
Matches	35;	Conservative	20;	Mismatches 38;
				Indels 5;
				Gaps 1

QY 7 FTTGLLLGASLLSLIGPQNVLVIKGGIKREGIALLVLCISDYFLFIAGTLGVDDLSMA 666
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 37 YLNGILVAAGLIITAIQAQNNFVLAOSLRREHHTLSVALCVFCDAVLVSLSVGFLAKILLE 966

QY 67 APIVDINRWGGLAYLLMFVNA-----AKDANTKYE 99
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
 Db 97 NPTLLAIRWGGIAFLTWYGLKALLRALRPPDALGNAAE 130

RESULT 6

Sequence 5737, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5737
LENGTH: 211
TYPE: PRT
ORGANISM: Acinetobacter baumannii
S-09-328-352-5737

Query Match 25.5%; Score 158; DB 2; Length 211;
 Best Local Similarity 32.6%; Pred. No. 3.3e-12;
 Matches 29; Conservative 25; Mismatches 35; Indels 0; Gaps 0;

QY 1 MWMEITITGLGASLLSIGPQNVLVKQIGREGIAVLVCLISDVFLFIAGTLGV 60
 DB 12 MSLSVFKEKIGIGSGIIVAGIAGNAFVLKQGLKQYVFWMLICALSDSLIACGVIGF 71

QY 61 DLSSNAPIVLDIRMGIAVLWFAVMA 89
 DB 72 AEIMTASPIITAKYIGATFLFYGAKA 100

RESULT 7
 US-09-902-540-9913
 ; Sequence 9913, Application US/09902540
 ; Patent No. 6833447
 ; GENERAL INFORMATION:
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15849)B
 ; CURRENT APPLICATION NUMBER: US/09/902,540
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 60/217,883
 ; PRIOR FILING DATE: 2000-07-10
 ; NUMBER OF SEQ ID NOS: 16825
 ; SEQ ID NO 9913
 ; LENGTH: 211
 ; TYPE: PRF
 ; ORGANISM: Myxococcus xanthus
 US-09-902-540-9913

Query Match 18.1%; Score 112; DB 2; Length 211;
 Best Local Similarity 25.6%; Pred. No. 3.1e-06;
 Matches 23; Conservative 26; Mismatches 35; Indels 6; Gaps 3;

QY 16 SLLSIGPQNVLVKQIGI---KREGIAVLVCLISDVFLFIAGTLGVDLSSAARIVD 72
 DB 17 ALITPPTPTMFLVLSKQGRKAGIVSALGI-FVGLFHIAAAGSLTSLATSLAPLS 75

QY 73 IMRWGIAVLWFAV--MAKADMTNKVEA 100
 DB 76 VVKMGGAAYLVWVGVMKRSKDTVAEAVQA 105

RESULT 8
 US-09-489-039A-7731
 ; Sequence 7731, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 7731
 ; LENGTH: 219
 ; TYPE: PRF
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-7731

Query Match 17.6%; Score 109; DB 2; Length 219;
 Best Local Similarity 27.9%; Pred. No. 8.1e-06;
 Matches 29; Conservative 20; Mismatches 45; Indels 10; Gaps 3;

QY 7 FITGLLAGSLLSIGPQNVLVKQIGI---REGIAVLVCLISDVFLFIAGTLGVDL 63

DB 17 YLYLVGAVRILLVPGNPFVLKGTIAGVKKGYLAAGV-FIGDAVLMFLAFAGVATL 75
 QY 64 SNAPIVLDIRMGIAVLW-----FAVMAKADMTNKVEAP 101
 DB 76 IKTPVLFVVRVYLGAIYLLMLGKMLYAVLITRDQSDASAP 119

RESULT 9
 US-09-543-681A-4767
 ; Sequence 4767, Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRAB.
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO 4767
 ; LENGTH: 212
 ; TYPE: PRF
 ; ORGANISM: Proteus mirabilis
 US-09-543-681A-4767

Query Match 16.0%; Score 99.5; DB 2; Length 212;
 Best Local Similarity 27.6%; Pred. No. 0.00013;
 Matches 27; Conservative 26; Mismatches 38; Indels 7; Gaps 3;

QY 5 EEIFGLLAGSLLSIGPQNVLVKQIGI---REGIAVLVCLISDVFLFIAGTLGV 61
 DB 17 DIFLSAIFSVTSITPGNNIMLASGINFGLKRTMPRAIGVSLGFFMLAVG-IGIG 75

QY 62 LLSNAPIVLDIRMGIAVLWFAVMAKADMTNKVE 99
 DB 76 ALIKSPITVNLKYLKALYLLM---LWKTAISHSVE 110

RESULT 10
 US-09-328-352-8249
 ; Sequence 8249, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 8249
 ; LENGTH: 235
 ; TYPE: PRF
 ; ORGANISM: Acinetobacter baumannii.
 US-09-328-352-8249

Query Match 15.1%; Score 93.5; DB 2; Length 235;
 Best Local Similarity 27.3%; Pred. No. 0.00092;
 Matches 33; Conservative 21; Mismatches 54; Indels 13; Gaps 5;

QY 3 IMEIFITGLGASLLSIGPQNVLVKQIGIKREGIAVLV---CLISDVFLFIAGTLG 59
 DB 29 LSQILAFGLIC-LAMVLTPGPMIYLLISRSIS-OGKIAGFISLGAVGFVYMLCASFG 86

QY 60 VDLSSNAPIVLDIRMGIAVLWFAVMAKADMTNKVEAPQIIEETPTVPDPTPLGV 119
 DB 87 ITALVAVPVYVITIRIAGAYLLMLMKLRP-----NAPLFNVKDLAV--DSPLKL 138

QY 120 F 120

[illegible]

RESULT 15
US-09-252-991A-18746
; Sequence 18746, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rudenfield et al.

```

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18746
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18746

```

```

Query Match      13.9%; Score 86; DB 2; Length 206;
Best Local Similarity 27.0%; Pred. No. 0.0072;
Matches 34; Conservative 17; Mismatches 51; Indels 24; Gaps 6;

QY      4 MEIFITGLLGASLLSLISGPONVLTIKQIKREGLIA---VLTVCILISDPFLFIAGTIG 59
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      10 MOSLVFPLFAVVASITPGFTNLTIVLSNS-QRHGLAAMPITVGCACAAVALIILIG-LG 67
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      60 VDLISNADPIVDIMRW---GGIAYLLMFAVMAAKDAMTNKVEAPQIIETEPTVPDDTP 116
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      68 LGELLRRHPLLOGLAMLVGWLSTYLAWSLFRSAGS-----IDGAEP---PRR 112
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      117 LGVFGG 122
      ||| ||| ||
DB      113 LGVLGG 118

```

Search completed: July 19, 2006, 00:32:11
 Job time : 52 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM proteoin - protein search, using sw model

Run on: July 19, 2006, 00:43:22 ; Search time 28 Seconds

(without alignments)
255.388 Million cell updates/sec

Title: US-10-716-470-10

Sequence: 1 MVMEIFITGLLAGSLLS.....EETEPVDDTPLGVFGGH 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 208217 seqs, 57668156 residues

Total number of hits satisfying chosen parameters: 208217

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA_New:
1: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US09_NEW_PUB.pep.*
2: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US06_NEW_PUB.pep.*
3: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US07_NEW_PUB.pep.*
4: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US08_NEW_PUB.pep.*
5: /EMC_Celerra_SIDS3/prodata/2/pubppaa/PCT_NEW_PUB.pep.*
6: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10_NEW_PUB.pep.*
7: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US11_NEW_PUB.pep.*
8: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101.5	16.4	205	6	US-10-471-571A-2892
2	91	14.7	226	7	US-11-056-355B-7128
3	91	14.7	250	7	US-11-056-355B-7127
4	89.5	14.4	452	7	US-11-199-489A-72
5	80	12.9	452	7	US-11-056-355B-5157
6	80	12.9	484	7	US-11-056-355B-5156
7	77.5	12.5	195	7	US-11-351-137A-2
8	75.5	12.2	597	6	US-10-449-902-53836
9	73	11.8	223	6	US-10-449-902-32208
10	73	11.8	594	6	US-10-449-902-38726
11	72.5	11.7	432	6	US-10-471-571A-8922
12	71	11.5	272	6	US-11-056-355B-24250
13	70.5	11.4	338	6	US-10-471-571A-4172
14	70	11.3	847	7	US-11-174-307B-70
15	69	11.1	271	7	US-11-056-355B-100151
16	69	11.1	294	7	US-11-056-355B-111390
17	69	11.1	294	7	US-11-056-355B-47598
18	69	11.1	294	7	US-11-056-355B-47597
19	69	11.1	357	7	US-11-056-355B-47596
20	67	10.8	255	7	US-11-056-355B-100153
21	67	10.8	255	7	US-11-056-355B-111392
22	67	10.8	255	7	US-11-056-355B-24251
23	67	10.8	264	7	US-11-056-355B-100152
24	67	10.8	264	7	US-11-056-355B-111391
25	67	10.8	361	7	US-11-331-549-5

26	66.5	10.7	423	7	US-11-056-355B-84175	Sequence 84175, A
27	66.5	10.7	146	6	US-10-471-571A-824	Sequence 824, App
28	66	10.6	466	6	US-10-449-902-40545	Sequence 40545, A
29	65.5	10.6	343	6	US-10-953-349-26206	Sequence 26206, A
30	65.5	10.6	343	7	US-11-056-355B-65566	Sequence 65566, A
31	65.5	10.6	359	7	US-11-056-355B-88538	Sequence 88538, A
32	65.5	10.6	359	7	US-11-056-355B-92294	Sequence 92294, A
33	65.5	10.6	403	6	US-10-471-571A-2714	Sequence 2714, App
34	65.5	10.6	635	7	US-11-056-355B-44864	Sequence 44864, A
35	65	10.5	222	6	US-10-953-349-34981	Sequence 34981, A
36	65	10.5	222	7	US-11-056-355B-4925	Sequence 4925, App
37	65	10.5	351	7	US-11-331-549-2	Sequence 2, Appl1
38	64.5	10.4	389	6	US-10-449-902-46963	Sequence 46963, A
39	64.5	10.4	792	6	US-10-449-902-53777	Sequence 53777, A
40	64.5	10.4	869	6	US-10-449-902-46963	Sequence 46963, A
41	64.5	10.4	1199	7	US-11-056-355B-83585	Sequence 83585, A
42	64.5	10.4	1213	7	US-11-056-355B-83584	Sequence 83584, A
43	64.5	10.4	1245	7	US-11-056-355B-83583	Sequence 83583, A
44	64	10.3	257	7	US-11-056-355B-23291	Sequence 23291, A
45	64	10.3	257	7	US-11-056-355B-74295	Sequence 74295, A

ALIGNMENTS

```

RESULT 1
US-10-471-571A-2892
Sequence 2892, Application US/10471571A
Publication No. US20060115490A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P02692700
CURRENT APPLICATION NUMBER: US/10/471,571A
PRIOR FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 2892
LENGTH: 205
TYPE: PRT
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(205)
OTHER INFORMATION: conserved hypothetical
US-10-471-571A-2892

Query Match      16.4% Score 101.5; DB 6; Length 205;
Best local Similarity 28.0%; Pred. No. 0.0013;
Matches 23; Conservative 20; Mismatches 36; Indels 3; Gaps 1;

QY      8  I T G L L G A S L L S I G P O N V L I K G I - - - K R E G L A V L V C L I S D V F L A G T L G V D L S 64
      6  I N F I L A I G L I P L G A Q N V F I N G A N Q K R Y V L P A I T T A G S D S L I I I A V G S I I I 65
      66 M S L P V L Q A I T Y V G L I F L M Y M A 87

DB      65 N A P I V L D I M R W G G A V L L M F A 86
      66 M S L P V L Q A I T Y V G L I F L M Y M A 87

RESULT 2
US-11-056-355B-7128
Sequence 7128, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nikolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
FILE REFERENCE: 2750-1590FUS2
CURRENT APPLICATION NUMBER: US/11/056,355B

```

```

; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; LENGTH: 226
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(226)
; OTHER INFORMATION: Ceres Seq. ID no. 12357352
US-11-056-355B-7128

```

```

Query Match      14.7%; Score 91; DB 7; Length 226;
Best Local Similarity 23.8%; Pred. No. 0.02;
Matches 25; Conservative 26; Mismatches 40; Indels 14; Gaps 5;

```

```

Qy      3 IMEFTITGLLGASLLSIGPQNVIVIKGIR--REGLIIVLVCLISDVFLFAGTIG 59
Db      105 IMPATITGLLIFMFLL-IATNMAIVSALMSLAAGFLAIFACVLA-VYI--GAVG 159

Qy      60 VDLISNAPIVLDIM-----RWGIIAYLWFAVMAAKDAMTKV 98
Db      160 VAIFAISAVISSVGVWITGWFVFWMIWFTARKSMDLTGHSI 204

```

```

RESULT 3
US-11-056-355B-7127
; Sequence 7127, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vvacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 7127
; LENGTH: 250
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(250)
; OTHER INFORMATION: Ceres Seq. ID no. 12357351
US-11-056-355B-7127

```

```

Query Match      14.7%; Score 91; DB 7; Length 250;
Best Local Similarity 23.8%; Pred. No. 0.02;
Matches 25; Conservative 26; Mismatches 40; Indels 14; Gaps 5;

```

```

Qy      3 IMEFTITGLLGASLLSIGPQNVIVIKGIR--REGLIIVLVCLISDVFLFAGTIG 59
Db      129 IMPATITGLLIFMFLL-IATNMAIVSALMSLAAGFLAIFACVLA-VYI--GAVG 183

Qy      60 VDLISNAPIVLDIM-----RWGIIAYLWFAVMAAKDAMTKV 98
Db      184 VAIFAISAVISSVGVWITGWFVFWMIWFTARKSMDLTGHSI 228

```

```

RESULT 4
US-11-199-489A-72
; Sequence 72, Application US/11199489A
; Publication No. US20060134745A1
; GENERAL INFORMATION:
; APPLICANT: Kluenhammer, Todd R.
; APPLICANT: Ruesell, William M.
; APPLICANT: Altermann, Eric

```

```

; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: TWO-COMPONENT SENSING AND REGULATORY PROTEINS, ANTIMICROBIAL
; FILE REFERENCE: 035051/295793
; CURRENT APPLICATION NUMBER: US/11/199,489A
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/599,972
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 452
; TYPE: prt
; ORGANISM: Lactobacillus acidophilus
US-11-199-489A-72

```

```

Query Match      14.4%; Score 89.5; DB 7; Length 452;
Best Local Similarity 22.4%; Pred. No. 0.065;
Matches 35; Conservative 29; Mismatches 39; Indels 53; Gaps 6;

```

```

Qy      7 FITGILLGASLL-----SIGPQNVIVIKO 31
Db      108 FVTGLITAILLIEFNPLHLGAKAATYODADFYRIISGAAPVFSIIPQN-LIRTE 166

Qy      32 GIKREGLIA-----VLVCLISDVFLF--AGTLGVDLISNAPIVLDIMRWGIIAYLW 85
Db      167 GLATQMIATMTGTITLAIIDPILFVFKGAIGVGIANITGYLTDL-----ILTY 218

Qy      86 AVMAAKDAMTKVKAPOIIEETPTVDDPPLGVFG 121
Db      219 YLCKTEYIKLKLKTKTKI---SGKTIKDVAIGIPG 251

```

```

RESULT 5
US-11-056-355B-5157
; Sequence 5157, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vvacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 5157
; LENGTH: 452
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(452)
; OTHER INFORMATION: Ceres Seq. ID no. 12409681
US-11-056-355B-5157

```

```

Query Match      12.9%; Score 80; DB 7; Length 452;
Best Local Similarity 27.5%; Pred. No. 0.7;
Matches 33; Conservative 19; Mismatches 40; Indels 28; Gaps 6;

```

```

Qy      14 GASLLSIGPQNVIVIKGIR--REGLIIVL-----LVCLISDVFLF-----IAGTLGVLD 62
Db      47 GSSDALQVTERILAVRACAEPRERLALDLAREDVACIVADAHLLTLTLDVARGLGVP 106

Qy      63 LSNAPIVLDIMRWGIIAYLWFAVMAA-----KQAMTKVKAPOIIEETPTVDDTP 116
Db      107 L-----VLRTGSAACLRMPAFAFPALCDKQVQPAQESQLBAP--VTLELPYRVADLP 155

```

```

RESULT 6
US-11-056-355B-5156

```

```

; Sequence 5156, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 5156
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(484)
; OTHER INFORMATION: Ceres Seq. ID no. 12409680
US-11-056-355B-5156

```

```

Query Match      12.8%; Score 80; DB 7; Length 484;
Best Local Similarity 27.5%; Pred. No. 0.76;
Matches 33; Conservative 19; Mismatches 40; Indels 28; Gaps 6;

```

```

QY 14 GASLLSISGPONLVIKQIK--REGLIIVL---LVCLISDVFL---IGTIGVYL 62
DB 79 GSSDALQVVERIVLANVRAEAPFRERLALAREVDACLVAAHALLTLIDVARGLGVP 138
QY 63 LSNAPDIVDIMRWGIAVYLLFPAVMAA-----KQAMTKVEAPQIIEETPTVPDTP 116
DB 139 L-----VLTGSAACLRMPAAPPALCDKGYQAPQESQLRP--VTLPYPRVADLP 187

```

```

RESULT 7
US-11-351-137A-2
; Sequence 2, Application US/11351137A
; Publication No. US20060148041A1
; GENERAL INFORMATION:
; APPLICANT: MAIER, THOMAS
; TITLE OF INVENTION: METHOD FOR FERMENTATIVE PRODUCTION OF AMINO ACIDS AND AMINO
; FILE REFERENCE: MAIER, T-2
; CURRENT APPLICATION NUMBER: US/11/351,137A
; PRIOR FILING DATE: 2006-02-09
; PRIOR APPLICATION NUMBER: GERMAN NO. 102 32 930.3
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-351-137A-2

```

```

Query Match      12.5%; Score 77.5; DB 7; Length 195;
Best Local Similarity 23.4%; Pred. No. 0.48;
Matches 29; Conservative 15; Mismatches 37; Indels 43; Gaps 5;

```

```

QY 3 IMEIFTGILLGASLLSISGPONLVIVI---KQIKRE-----GLIIVLVCLISD 49
DB 5 LLSAFTVYTLIRH--MTGPNHILALSSATSGFRGOSRVLGMSLGLIYVLLCADIS 61
QY 50 VFLFAGTIGVLLSNAPDIVDIMRWGIAVYLLFPAVMAAKDAMTKVEAPQIIEETPT 109
DB 62 FSLAVIDPAVAVHLS-----WAGAAVYIVLAWKIA-----TSP 94
QY 110 TVPD 113
DB 95 TKED 98

```

```

RESULT 8
US-10-449-902-53836
; Sequence 53836, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 53836
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53836

```

```

Query Match      12.2%; Score 75.5; DB 6; Length 597;
Best Local Similarity 20.8%; Pred. No. 3;
Matches 30; Conservative 22; Mismatches 53; Indels 39; Gaps 4;

```

```

QY 12 LIGASLLSISGPONLVIKQIKREGLIIVLVCLISDVFLFAGTIGVYLLSNAPIVYL 71
DB 197 VLGSAMLVSSAVLGVGVGLGARG--VAVRDVDFRDSFLAALAAVAVLAAGEVTI 253
QY 72 DIMRWGIAVYLLFPAVMAAKDAMTN-----KVEAPQIIEETPT 108
DB 254 ---WGALAFSTLYVYVVAFAVTHGRAPSKGAGADHTADAFSELGVATKFFYGDGE 309
QY 109 PTVPPDTPV-----GVFGGG 123
DB 310 PLLPDTAPLLSYYPGGDGGGGGG 333

```

```

RESULT 9
US-10-449-902-33208
; Sequence 33208, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 33208
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-33208

```

```

Query Match      11.8%; Score 73; DB 6; Length 223;
Best Local Similarity 23.5%; Pred. No. 1.7;
Matches 24; Conservative 24; Mismatches 40; Indels 14; Gaps 5;

```

```

QY 6 IFITGILLGASLLSISGPONLVIKQIK--REGLIIVLVCLISDVFLFAGTIGVYL 62

```

Db 105 IATGLIFMPELL-VATTNAVVSVMLSLAAGSFLMFACLVA-VYI---GVVSVAV 159
 QY 63 LSNAPVLDIM-----RMGIAVLMFAVMAKADANTKV 98
 Db 160 FVISAIVISAIVGVMIATGMLGFFFMIMFAARKSDLTKHSI 201

RESULT 10
 US-10-449-902-38726
 ; Sequence 38726, Application US/10449902
 ; Publication No. US20060123505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agricultural Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-A0205Y1-US
 ; CURRENT APPLICATION NUMBER: US/10/449,902
 ; PRIOR FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIOR FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: Patent Ver. 2.1
 ; SEQ ID NO 38726
 ; LENGTH: 594
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; US-10-449-902-38726

Query Match 11.8%; Score 73; DB 6; Length 594;
 Best Local Similarity 29.6%; Pred. No. 5.5;
 Matches 29; Conservative 14; Mismatches 29; Indels 26; Gaps 6;

QY 4 MEIFITGLLIGASLLSLISGPONVVIKQIKREGIAVLV-----CLISD-----V 50
 Db 192 LSLFVAGYGLGPILM---GP-----LSQYGRPVFIQAMLVYCFNIGCALSKRTGSLV 244
 QY 51 FLFIAGTGLVDLSNAPVLDIMRWG---GIAYLIW 84
 Db 245 FRFLAGTFASPLTNSGVYIDL--WDKTRGIALSLF 280

RESULT 11
 US-10-471-571A-822
 ; Sequence 822, Application US/10471571A
 ; Publication No. US20060115490A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SpA
 ; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE: P026927WO
 ; CURRENT APPLICATION NUMBER: US/10/471,571A
 ; CURRENT FILING DATE: 2003-09-12
 ; PRIOR APPLICATION NUMBER: GB-0107661.1
 ; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 5642
 ; SOFTWARE: Seqwin99, version 1.03
 ; SEQ ID NO 822
 ; LENGTH: 432
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (1)..(432)
 ; OTHER INFORMATION: aeenical pump membrane
 ; US-10-471-571A-822

Query Match 11.7%; Score 72.5; DB 6; Length 432;
 Best Local Similarity 31.1%; Pred. No. 4.3;
 Matches 23; Conservative 7; Mismatches 19; Indels 25; Gaps 3;

QY 19 LSTIGPONVVIKQIKREGIAVLVCLISDVFLIAGTGLVDLSNAPVLDIMRWG 78
 Db 350 IALGOSNV---HGMLEGLI-----YANVIGSDLGPKITPI-----GS 384
 QY 79 IAYLMEFAVMAKD 92
 Db 385 LATLMLHVLTKQD 398

RESULT 12
 US-11-056-355B-24250
 ; Sequence 24250, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brover, Vyacheslav
 ; APPLICANT: Alexandrov, Nikolai
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT APPLICATION NUMBER: US/11/056,355B
 ; CURRENT FILING DATE: 2005-02-14
 ; PRIOR APPLICATION NUMBER: 60/544,190
 ; PRIOR FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO 24250
 ; LENGTH: 272
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: peptide
 ; LOCATION: (1)..(272)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12321538
 ; US-11-056-355B-24250

Query Match 11.5%; Score 71; DB 7; Length 272;
 Best Local Similarity 28.5%; Pred. No. 3.6;
 Matches 37; Conservative 23; Mismatches 50; Indels 20; Gaps 7;

QY 7 FITGL-----LIGASLLISGPONVVIKQIKREGIAVLVCLISDVFLIAGTGLV 60
 Db 7 FVAGLNTLWLVGAS---AIGSIYMFVHQGV-IDCESAIRIPLTTGLIFLVSILGV 62
 QY 61 --DLSNAPVLDIMRWGIAVLLMFAVMAKADMTKVEAPDIE---ETEPVVD 113
 Db 63 IGSCKENLAMSYYLILFGIYALMTISIFL--FVTK-GGRVSGRGKYKRTVD 119
 QY 114 DTPLGVFGG 123
 Db 120 STWLNGFVG 129

RESULT 13
 US-10-471-571A-4172
 ; Sequence 4172, Application US/10471571A
 ; Publication No. US20060115490A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SpA
 ; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE: P026927WO
 ; CURRENT APPLICATION NUMBER: US/10/471,571A
 ; CURRENT FILING DATE: 2003-09-12
 ; PRIOR APPLICATION NUMBER: GB-0107661.1
 ; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 5642
 ; SOFTWARE: Seqwin99, version 1.03
 ; SEQ ID NO 4172
 ; LENGTH: 338
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (1)..(338)

OTHER INFORMATION: ferrichrome transport
US-10-471-571A-4172

Query Match 11.4%; Score 70.5; DB 6; Length 336;
Best Local Similarity 24.5%; Pred. No. 5.3;
Matches 25; Conservative 22; Mismatches 40; Indels 15; Gaps 3;

QY 1 MWMEIFITGLLIGASLLISGPONVLY-----IKQIKREGIIV-----LVLCL 47
DB 11 LILAVFSILFLPGCTWSITSGEYNIPEPFKTLICQDAIDELLDLPRLPMTITL 70
QY 48 SDVFLIAGTGLGDLSSN--AAPIVLDIMMGIAVLLMFAV 87
DB 71 AGAALISGAIVOSVTKNPIAEPIIGINAGGFALMFLAI 112

RESULT 14
US-11-174-307B-70

Sequence 70, Application US/11174307B
Publication No. US20060143729A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 2750-1601PUS2
CURRENT APPLICATION NUMBER: US/11/174,307B
CURRENT FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: 60/583,671
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/583,781
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/583,651
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 5544
SEQ ID NO 70
LENGTH: 847
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: OTHER INFORMATION: Pfam Name: Na_H_Exchange; Pfam Description: Sodium/hydrogen
FEATURE:
NAME/KEY: misc_feature
LOCATION: OTHER INFORMATION: GI Number: 6692096; NR Description: F22C12.7 (Arabidopsis thaliana)
FEATURE:
NAME/KEY: misc_feature
LOCATION: OTHER INFORMATION: GI Number: 9294151; NR Description: Na+/H+ exchange
FEATURE:
NAME/KEY: misc_feature
LOCATION: OTHER INFORMATION: GI Number: 15128390; NR Description: P0454H12.8 (Oryza sativa)
FEATURE:
NAME/KEY: misc_feature
LOCATION: OTHER INFORMATION: GI Number: 61658325; NR Description: cation/H+ exchanger
US-11-174-307B-70

Query Match 11.3%; Score 70; DB 7; Length 847;

Best Local Similarity 24.6%; Pred. No. 18;
Matches 32; Conservative 23; Mismatches 53; Indels 22; Gaps 5;

QY 4 MEIFITGLLIGASLLISGPONVLYIKQIKREGIIVLVLISDVFLIAGTGLGVDL 63
DB 356 IEDLVMGILLPLVYFMS-GLKTDITTIQGVKSGKRLALVY---TACFGKIVGVSVALL 411

QY 64 SNA---APIVLDI--MEWGGIAVLL-----WEAVMAAKDAMTKVEAPOIE 105
DB 412 CKRLAESVLSGLVMTTKGLVELIVINICKDKRVISDQFFAIVMAAIFTTFTTPIVLA 471
QY 106 ETEPTVDDT 115
DB 472 LYKPSSTQT 481

RESULT 15

US-11-056-355B-100151
Sequence 100151, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nikolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 100151
LENGTH: 271
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(271)
OTHER INFORMATION: Ceres Seq. ID no. 13604468
US-11-056-355B-100151

Query Match 11.1%; Score 69; DB 7; Length 271;
Best Local Similarity 28.5%; Pred. No. 5.9;
Matches 37; Conservative 23; Mismatches 50; Indels 20; Gaps 7;

QY 7 FITGL-----LIGASLLISGPONVLYIKQIKREGIIVLVLISDVFLIAGTGLV 60
DB 7 FVWGLANTLVMLVGS--AIGSYIMFVHGV--TDCSAIRIPLLTTGLILFLVSLGLV 62
QY 61 ---DLISNAAPVIDIMMGIAVLLPFAVMAAKDAMTKVEAPOIE---ETEPTVDD 113
DB 63 IGSCFKELAMVSKYIILIFGSIVALMTFSIFL--FVINK-GAGRVVSGRGYKERTVD 119
QY 114 DPLGVFGG 123
DB 120 STWLNGFVGG 129

Search completed: July 19, 2006, 00:46:52
Job time : 29 secs